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151 GAGGAGTTTGAGACCCGCTTCGGCGCACCTTCTGACCTGCCGCTCA 200
67 nleuHISValThrProGlySerAlaGlnAlaInArgPheThrGlnValSera 84
201 GCTACAGCTGACCCAGGCTCAGCCAGCCAGCACGCTTCAACCCAGGTTCCG 250
84 spgIleuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
251 ACGAACCTTTCCAGGGGGGCCCACTGGGCGCTTGTGGCATCTTT 300
101 ValPheGlyAlaAlaLeuGlyAlaGlnSerValAlaAsnLysGluMetGluPr 117
301 GTCTTGGGGGCTGCCCTGTGTCTGAGAGTGTCAACAAGAAATGAGACC 350
117 oleuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
351 ATTGGTGGGACAAGTGCAGAGATTGGATGTGACCTGAGAGACAGCT 400
134 euAlaAspTrpIleHisSerSerGlyGlyTyrPalaGluPheThrAlaLeu 150
401 TGGCTGACTGGATCCACAGACAGTGGGGCTGGCGGAGTTCCACAGCTCTA 450
151 TyrGlyAspGlyAlaLeuGluGlnAlaArgArgLeuArgGluGlyAsnTr 167
451 TACGGGGAGCGGGCCCTGGAGAGGACGCGCTGTGCGGGAGGGAACGTG 500
167 PalaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
501 GCCATCAGTAGAGACAGTGTGACGGGGGCTGTGCGACTGGGGGCCCTGG 550
184 alThrValGlyAlaPhePheAlaSerLys 193
551 TAACGTAGGGGCTTTTTCCTAGCAAG 579

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seq_name: /cgn2_6/prodata/1/ina/5B_COMB.seq:us-08-978-523-1

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seq_documentation_block:
; Sequence 1, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; US-08-978-523-1

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alignment_scores:
Quality: 1002.00 Length: 193
Ratio: 5.192 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 98.964

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alignment_block:

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Align seg 1/1 to: US-08-978-523-1 from: 1 to: 579

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17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
51 TGTAGGCTATAGCTGAGACAGAGGGTATGTCTGTGAGCTGGCCCTG 100
34 LysGlyLysProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
101 GGGAGAGCCAGCAGCCGACCCGCTGCACCAACCCATGCGGCGACTGGA 150
51 AspGluPheGluThrArgPheArgThrPheSerAspLeuAlaAlaG 67
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67 nleuHISValThrProGlySerAlaGlnAlaInArgPheThrGlnValSera 84
201 GCTACAGTGCACCCAGGCTCAGCCAGCCAGCACGCTTACACAGGTTCCG 250
84 spgIleuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
251 ACGAACCTTTCCAGGGGGGCCCACTGGGCGCTTGTGGCATCTTT 300
101 ValPheGlyAlaAlaLeuGlyAlaGlnSerValAlaAsnLysGluMetGluPr 117
301 GTCTTGGGGGCTGCCCTGTGTCTGAGAGTGTCAACAAGAAATGAGACC 350
117 oleuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
351 ATTGGTGGGACAAGTGCAGAGATTGGATGTGACTGAGAGACAGCT 400
134 euAlaAspTrpIleHisSerSerGlyGlyTyrPalaGluPheThrAlaLeu 150
401 TGGCTGACTGGATCCACAGACAGTGGGGCTGGCGGAGTTCCACAGCTCTA 450
151 TyrGlyAspGlyAlaLeuGluGlnAlaArgArgLeuArgGluGlyAsnTr 167
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167 PalaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
501 GCCATCAGTAGAGACAGTGTGACGGGGGCTGTGCGACTGGGGGCCCTGG 550
184 alThrValGlyAlaPhePheAlaSerLys 193
551 TAACGTAGGGGCTTTTTCCTAGCAAG 579

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seq_name: /cgn2_6/prodata/1/ina/5A_COMB.seq:us-08-798-897-2

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seq_documentation_block:
; Sequence 2, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John

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TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
 TITLE OF INVENTION: Homologue
 NUMBER OF SEQUENCES: 53
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 STREET: 1100 New York Avenue, N.W., Suite 600
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/798,897
 FILING DATE: February 11, 1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Esmond, Robert W.
 REGISTRATION NUMBER: 32,893
 REFERENCE/DOCKET NUMBER: 1483.0140001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 579 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 MOLECULE TYPE: cDNA
 US-08-798-897-2

alignment_scores: Length: 193
 Quality: 992.00 Gaps: 0
 Ratio: 5.167
 Percent Similarity: 99.482 Percent Identity: 97.927

alignment_block:
 US-09-155-327E-9 x US-08-798-897-2 ..

Align seg 1/1 to: US-08-798-897-2 from: 1 to: 579

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17 eValaGlyTArgLeuArgInlysglyTyrValcysGlyAlaGlyProg 34
17 |||||||.....:|||||.....:|||||.....:|||||.....:
51 TGTAGTTATTAAGCTGAGCAGAGAGGTTTGTCTGTGGAGCTGGCCCG 100
34 lYcGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
34 |||||||.....:|||||.....:|||||.....:|||||.....:
101 GGGAGGGCCCGACCTGACCTGCACCAAGCATGGCGGAGCTGGA 150
51 AspGluPheGluThrArgPheArgThrPheSerAspLeuAlaAlaGly 67
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67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
67 |||||||.....:|||||.....:|||||.....:|||||.....:
201 GCTGCATGTACCCAGGCTCAGCCCAACACAGCTTCAACCAAGGCTCCG 250
84 spGluLeuPheGlnGlyGlyProAsnTyrGlyArgLeuValAlaPhePhe 100
84 |||||||.....:|||||.....:|||||.....:|||||.....:
251 ATGAACATTTTCAAGGGGGCCCAACTGGGGCGGCTTGTACCTTCTTT 300
101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnIlysgluMetGluP 117
101 |||||||.....:|||||.....:|||||.....:|||||.....:
301 GTCTTTGGGCTGCACCTGTGTGCTGAGAGTGTCAACAGAGATGGAAAC 350
  
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117 oleuValGlyGlnValGlnAspTTPMeValAlaTyrLeuGluThrArgL 134
117 |||||||.....:|||||.....:|||||.....:|||||.....:
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seq_name: /cgn2_6/ptodata/1/lna/5B_COMB.seq:US-08-978-523-2

seq_documentation_block:
 : Sequence 2, Application US/08978523
 : Patent No. 5883229

GENERAL INFORMATION:

Applicant: Guastella, John

TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2

TITLE OF INVENTION: Homologue

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/978,523

FILING DATE: herewith

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/798,897

FILING DATE: February 11, 1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 1483.0140002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 579 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: cDNA

US-08-978-523-2

alignment_scores: Length: 193
 Quality: 992.00 Gaps: 0
 Ratio: 5.167
 Percent Similarity: 99.482 Percent Identity: 97.927

alignment_block:

US-09-155-327E-9 x US-08-978-523-2

Align seg 1/1 to: US-08-978-523-2 from: 1 to: 579

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1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAsp 17
1 ATGGGAGCCCGACCTCGGCCCGACAGACACAGGGCTCTGTTGAAACACT 50
17 eValAlaThrArgLeuArgGlnLysGlyValAlaCysGlyAlaGlyPro 34
1 TGTAGTTATAGCTGAGGCGGAGAGGGTTATGCTGTGGAGCGTGGCCCG 100
34 LysGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
101 GGGAGGCGCCAGCAGCTGACCCACCTGACCAACCATGGGGCAGCTGA 150
51 AspAlaPheGlnThrArgPheArgThrPheSerAspLeuAlaAlaG 67
151 GATGAGTTCGAGACCCGCTCCGGCCACTTCTCTGATCTGGCGCTCA 200
67 nLeuHisValThrProGlySerAlaGlnAlaArgPheThrGlnValSera 84
201 GCTGCATGTACCCAGCTGACGCCCAACACAGCTTCCACCCAGGCTCCG 250
84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
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101 ValPheGlyAlaAlaLeuCysAlaGlnSerValAsnLysGlnMetGly 117
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151 TyrGlyAspGlyAlaLeuGlnGlnAlaArgArgLeuArgGlnGlyAsnTr 167
451 TACGGGGAGGGGGCGCTGGAGAGCGGGCGCTGCGGGAGGGAACTG 500
167 PalSerValArgThrValLeuThrGlyAlaValAlaLeuGlnAlaLeu 184
501 GGCATCAGTACAGAGACGTGTCAGGGGCGCTGGCAGCTGGGGCCCTG 550
184 alThrValGlyAlaPhePheAlaSerLys 193
551 TAACTGTAGGGGCTTTTGTCTACCAAG 579

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seq_name: /cgn2_6/ptodata/1/ina_5A_COMB.seq:US-08-081-448-5

seq_documentation_block:

Sequence 5, Application US/08081448
 Patent No. 5646008
 GENERAL INFORMATION:
 APPLICANT: Thompson, Craig B.
 APPLICANT: Boise, Lawrence H.
 TITLE OF INVENTION: Vertebrate Apoptosis Gene:
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Arnold, White & Durkee
 STREET: 321 No. 3646008th Clark Street, Suite 800
 CITY: Chicago
 STATE: IL
 COUNTRY: USA
 ZIP: 60610
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/081,448
 FILING DATE: 19930622
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
 NAME: No. 5646008thrup, Thomas E.
 REGISTRATION NUMBER: 33,268
 REFERENCE/DOCKET NUMBER: ARCD090
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-744-0090
 TELEFAX: 312-755-4489
 INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
 LENGTH: 926 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:

NAME/KEY: CDS
 LOCATION: 135..836
 US-08-081-448-5

alignment_scores:

Quality: 424.50 Length: 224
 Ratio: 2.989 Gaps: 4
 Percent Similarity: 63.393 Percent Identity: 40.179

alignment_block:

US-09-155-327E-9 x US-08-081-448-5

Align seg 1/1 to: US-08-081-448-5 from: 1 to: 926

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200 CAGCTGAGTCACTTATGATGTGAAGAGAACAGACTGAGCCCGCAG 249
28 .....:|||||.....:|||||.....:|||||.....: 250
250 AAGGACTGATCGAGATGAGAGACCCAGTGCCTCATTAATGCAACCA 299
34 .....:GlyGlnGlyProAlaAlaAsp.....:|||||.....: 40
300 TCTGGACACTGGCAGACAGCCCGCGGTGATGAGACCACTGCGCACAG 349
41 .....:|||||.....:|||||.....:|||||.....: 350
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45 lametargAlaAlaGlyAspGlnPheGlnThrArgPheArgThrPhe 61
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62 SerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGln 78
450 |||||.....:|||||.....:|||||.....:|||||.....: 499
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78 gPheThrGlnValSerAspGlnLeuPheGlnGlyGlyProAsnTrpGly 95
500 |||||.....:|||||.....:|||||.....:|||||.....: 549
500 CTTGAAACAGGTAGTGAATGAATCTTCCGGATGGGTAAACTGGGGTC 549
95 rGlnValAlaPhePheValPheGlyAlaAlaLeuCysAlaGlnSerVal 111
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Percent Similarity: 63.393      Percent Identity: 40.179

Alignment block:
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27 T..... 27
200 CACCTGGAGTCACTTTAGTGAATGTGGAAGAGAACAAGACTAGAGCCCA 249
   ||| |||||:|||||:|||||:||||| ValCysGlyValaGlyPro 33
28 ..... 28
250 AAGGAGCTGAATCGAGAGATGGAGACCCCAAGTCGATCAATGGCAACCA 299
   ||| |||||:|||||:|||||:||||| GlyGluGlyProAlaAlaAsp..... 40
34 ..... 34
300 TCCTGGACCTGGAGACAGACCCCGCGGTGAATGGAGACCACTGGCAAG 349
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41 ..... 41
350 CAGCAGTTTGGATGCCGGGAGAGTGAATCCCAATGGACAGCAAGTAAACAG 399
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45 IAmelArgAlaAlaGlyAspGlyRheGlyThrArgRheArgArgTyrPhe 61
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62 SerAspLeuAlaAlaGlnLeuHisValaThrProGlySerAlaGlnGlnAr 78
450 AGTGACCTGACATCTCCAGCTCACATCCCAAGGAGGACAGCATGTACAGAG 499
78 gPheThrGlnAlaSerAspGlyLeuPheGlnGlyGlyProAsnThrLeuA 95
500 CTTTGACACGATGATGATGAATGAATCTTCCGGGATGGGGTAAACTGGGCTC 549
95 rGleuValAlaPheRheValaRheGlyValaAlaLeuCysAlaGlnSerVal 111
550 GCATTTGTGGCTTTTCTCTCTTCCGGCGGGGCACTGTGGCTGGAAAGCGTA 599
112 AsnLySGlnMetGlyProLeuValaGlyGlnValaGlnAspTrpMetValAl 128
600 GACAGAGAGATGGAGGTATGTGGAGTCGAGATCGACGCTGTGATGGCCAC 649
128 aTyLeuGluThrArgLeuAlaAspTrpLeuHisSerSerGlyGlyTPA 145
650 TTACCTGGAAGACCACTTGAAGCCTTGATCCAGAGAAAGCGGCGCTGG 699
145 IagIupheThrAlaLeuTyGlyAspGlyAlaLeuGlnAlaArgArg 161
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162 LeuArgGlu..... GlyAsnTrpAlaSerValaArgThrValaLeuThrG 176
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seq_name: /cgn2_6/prodata/1/lna/6A_COMB.seq:US-08-481-739-1
seq_documentation_block:
; Sequence 1, Application US/08481739
; Patent No. 6143291
; GENERAL INFORMATION:
; APPLICANT: June, Carl H. and Thompson, Craig B.
; TITLE OF INVENTION: METHODS FOR ENHANCING T CELL SURVIVAL
; TITLE OF INVENTION: BY AUGMENTING BCL-XL PROTEIN LEVELS
; NUMBER OF SEQUENCES: 4

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27 T.....
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41 ..... ProLeuHisGlnA 45
350 CAGCAGTTTGGATCCCGGAGAGTGATCCCATAGCAGCAGTAAACCAAG 399
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550 GCATGTGGCTTTTCTCTTCCTCGCGGGGACAGTGGTGGAAGGGTA 599
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650 TTACCTGAATGACCACTAGACCTTGGTGGTCAGAGAACGGCGCTGG 699
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seq_documentation_block:
; Sequence 39, Application US/09277020
; Patent No. 6210892
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
; FILE REFERENCE: ISPH-0339
; CURRENT APPLICATION NUMBER: US/09/277,020
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 09/167,921
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; TYPE: DNA
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% ORGANISM: Homo sapiens
US-09-277-020-39

alignment_scores:
    Quality: 424.50      Length: 224
    Ratio: 2.989         Gaps: 4
    Percent Similarity: 63.393      Percent Identity: 40.179

alignment_block:
US-09-155-327E-9 x US-09-277-020-39 ..

Align seg 1/1 to: US-09-277-020-39 from: 1 to: 926

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150 CGGAGCTGGTGGTGTGACTTCTCTCTACAGAGCTTCCGAGAAAGGATA 199

27 T..... 27
   |
200 CAGCTGAGTCACTTTAGTAGTGTGAGAGAACAGACGACTGAGGCCACG 249
   .....ValcysglyAlaGlyPro 33
28 .....::: :::::||||
250 AAGGACTGAATCGAGATGAGAACCCCAAGTGCATCAATGAGCAACCA 299
34 .....glyGlnGlyProAlaAlaAsp..... 40
300 TCTGCGACACTGTCGAGACAGCCCGCGGTGAATGAGAGCCACTGCGCACG 349
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41 .....ProLeuHisGlnA 45
350 CAGCAGTTTGGATGCCCGGAGGTGATCCCATGSCACACAGTAAAGCAAG 399
45 IAmETArgAlaAlaGlyAspGlnPheGluThrArgPheArgThrPhe 61
   ||:::|||| |||||:::|||||:::|||||:::|||||:::|||||
400 CCCTGAGGAGGAGCAGCGACGCGATTGAACCTGCGTACCGCGGCGCATTC 449
62 SerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGlnAr 78
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78 gPheThrGlnAlaSerAspGlnLeuPheGlnGlyGlyProAsnTrpGlyA 95
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95 rGLeuValAlaPhePheValPheGlyAlaAlaLeuGlnSAlaGlnSerVal 111
550 GCATTTGTGCGCTTTTCTCTCTCGGGGAGCACTGTGCGGGAACGTA 599
112 AsnIysGlnMetGluProLeuValAlaGlyGlnValAlaAspTrpMetValAl 128
600 GACAAGAGAGTGCAGGTATTTGTGCACTGGATGCGACGCTTGATGGAGCCAC 649
128 aTyrlLeuGluThrArgLeuAlaAspTrpIleHisSerSerGlyGlyTyrA 145
650 TTACCTCAATGACACCACTAGAGCCTTGGAACTCAGAGAACGGCGGCTGGG 699
145 IaGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGlnGlnAlaArgArg 161
700 ATACTTTGTGGAACCTTATGGGAAACAATGACAGCAGCGAGAGCGAAG 749
162 LeuArgGlu.....GlyAsnTrpAlaSerValArgThrValLeuThrG 176
   ::||| :::::|||| ::: :::::||||
750 GGCACGAGAGCGCTTCAACCGCGCTTCTCGACGGGACATGACTGTGGCGG 799
176 yAlaValAlaLeuGlnGlyAlaLeu 183
800 CGTGTTCTGCTGGGCTCAGTC 821

seq_name: /cgn2_6/prodata/1/lna/6B_COMB.seq:US-09-323-743-1
seq_documentation_block:

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alignment_scores:
Quality: 424.50
Length: 22

•

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/228,704
FILING DATE: 18-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 994,941
FILING DATE: 23-DEC-1992
APPLICATION NUMBER: 663,010
FILING DATE: 19-MAR-1991
APPLICATION NUMBER: 883,687
FILING DATE: 09-JUL-1986
SEQ ID NO: 1
LENGTH: 4825
5459251-1

alignment_scores:

Quality: 406.50 Length: 235
Ratio: 2.904 Gaps: 5
Percent Similarity: 59.574 Percent Identity: 36.596

alignment_block:

US-09-155-327E-9 x 5459251-1 ..

Align seg 1/1 to: 5459251-1 from: 1 to: 4825

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9 AspThrArgAlaLeuValAlaAspPheValGlyTrpArgLeuArgGly 25
|||||
1486 GACACCCGGGAGATAGTGTAGTACATCATTAAGCTGCGCAGAG 1535
25 sGLyTrpValCysGlyAlaGly..... 32
|||||
1536 GGGGTACGAGTGGGTGGGAGATGGGGCGCGCGCGGGGGCGG 1585
33 .....ProGlyGlu..... 35
|||||
1586 CCCCCGACCGGCACTTCTCTCCAGCCGGGACACGCCCATCA 1635
35 ..... 35
1636 GCCGATCCCGGACCGGTCGCCAGGACCTGCCGCTGCAGACCCGGC 1685
36 .....GlyProAlaAlaAspPro.....L 42
|||||
1686 TGCCCCCGGCGCCCGCGGGCTGCGCTACGCCGCTGCACCTGTGG 1735
42 euHisGlnAlaMetArgAlaAlaGlyAspGluPheGluTrpArgPheArg 58
|||||
1736 TCCACCTGGCCCTCCGCCAAGCCGGCGACCTTCTCCGCCGCTACCGC 1785
59 ArgThrPheSerAspLeuAlaAlaGlnLeuHisValThrProGlySerAl 75
|||||
1786 GCGGACTTCCCGGAGATGTCAGGACACCTGACGCTTCAACCGC 1835
75 aGlnGlnArgPheThrGlnValSerAspGluLeuPheGlnGlyPro 92
|||||
1836 GCGGGGACGCTTGGCACGCTGGTGGAGAGCTTTCAGGGGCGGGGTGA 1885
92 snTrpGlyArgLeuValAlaPhePheValPheGlyAlaAlaLeuCysAla 108
|||||
1886 ACTGGGGAGAGATTGGCTCTTGGAGTGGTGGGTGATGTGTG 1935
109 GluSerValAsnLysGluMetGluProLeuValGlyGlnValGlnAspTr 125
|||||
1936 GAGAGCGTCAACCGGAGATGCGCCCTGGTGACACATCGCCCTGTG 1985
125 pMetValAlaTrpLeuGluTrpArgLeuAlaAspTrpIleHisSerSerG 142
|||||
1986 GATGACTGATGACTGACACCGGACCTGCACACTGATCCAGGATACG 2035
142 LysGlyTrpAlaGluPheThrAlaLeuTrpGlyAspGlyAlaLeuGluGln 158
|||||
2036 GAGGCTGGGATGCTTGTGAACTGTACGCG.....CCGACG 2073
```

```
159 AlaArgArgLeuArgGluGlyAsnTrpAlaSerValArgThrValLeuTrh 175
|||||
2074 ATGGGCGCTCTGTGTTGATTCTCCTGGCTGCTCTGAAAGACTGCTCAG 2123
175 rGlyAlaValAlaLeuGlyAlaLeuValThrValGlyAlaPhePheAla 192
|||||
2124 TTGGCCCTG...GTGGAGCTTGCATCACCTGGTGGCTATCTGAGCC 2170
192 eRLys 193
|||||
2171 ACAAG 2175
```


•
•
•
•

•

•

17 evalgIyTyrArgIeulArgIuIySGIyTyrAlaIySGIyAlaGIyProG 34
182 TGTAGGCTTAAGCTGATGAGCAAGAGGTTATCTGTGTGAGCTGGCCCTG 233
34 IyGIuGIyTroAlaAlaAspProIeuuHISGInAlaMetArgAlaAlaGIy 50
232 GGGAAAGGCCACCCGCCGACCCGCTGACCAAGCCATCGGGGCTGTGA 283
51 AspGIuPheGIuThrArgPheArgArgIhrPheSerAspLeuAlaAlaGI 67

TITLE
Iinoda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN Integrated Sequence Analysis (RISA) Project

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
1 (bases 1 to 1030)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cga@pds-remail.nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution by: Incyte Genomics, Inc.
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM800 row: p column: 04
High quality sequence start: 5
High quality sequence stop: 709.

FEATURES

source

1..1030
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:394307"
/clone_lib="NIH-MGC.7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/note="Organ: Lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT
190 a 284 c 386 g 170 t
ORIGIN

alignment_scores:

Quality: 945.00 Length: 190
Ratio: 5.027 Gaps: 1
Percent Similarity: 98.947 Percent Identity: 95.789

Alignment block:

US-09-155-327E-9 x BE793530 ..

Align seg 1/1 to: BE793530 from: 1 to: 1030

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1 MetalaThrProAlaSerThrProAspThrArgAlaLeuValAlaAsp 17
|||||
144 ATGGGACCCAGCCCTGGCCCGACACACAGGCGCTCTGTGCGACACT 193
17 eValGlyTyrArgLeuArgGlnGlyTyrValGlyGlyAlaGlyProG 34
|||||
194 TGTAGGTTATAGCTGAGCGAGAGAGGCTATGTCTGTGAGCGCTGGCC 243
34 TgtGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
|||||
244 GGGAGGCGCCAGCAGCTGACCCAGTGCACCAACCATGGGGAGCTGGA 293
51 AspGluThrGluThrArgPheArgArgThrPheSerAspLeuAlaGly 67
|||||
294 GATGAGTTTCAGACCCGCTCCGGCCACCTTCTGATCTGGCGGCTCA 343
67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSer 84
|||||
344 GCTGCATGTACCCAGCTCAGCCCAACACAGCTTACCCAGGCTCCG 393
84 spGluThrPheGlnGlyProAsnTTPGlyArgLeuValAlaPhePhe 100
|||||
394 ATGAACCTTTTCAAGGGGCGCCCAACTGGGCGGCTGTGACCTTCTTT 443

```

101 ValPheGlyAlaAlaLeuGlyAlaGlnSerValAlaGlnGlyMetGluP 117
|||||
444 GCTCTTGGGGCTGACCTGTGCTCAGAGTGTCAACAAGAGAGTGAAC 493
117 oLeuValGlyGlnValGlnAspThrMetValAlaTyrLeuGluThrArg 134
|||||
494 ACTGGTGGACACAGTGCAGAGTGTGCTGCTACTGAGACGGGGC 543
134 eValAspThrPheHisSerSerGlyGlyTyrPalaGluPheThrAlaLeu 150
|||||
544 TGGCTGACTGATCCACAGCAGTGGGCGTGGGGGAGTTACACAGCTCTA 593
151 TyrGlyAspGlyAlaLeuGluGlnAlaArgArgLeuArgGlnGlyAsn 167
594 TACGGGAGCGGGCGCTGGAGAGAGCCCGCTCTCGGGAGGAGCTG 643
167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeu 183
|||||
644 GCATCAGTGCAGACAGTGTGCTGACGGGGCGCTGCGACTGGGGGCTCG 693
184 ValThrValGlyAlaPhe 189
|||||
694 GTAACGTAGGGGCTTT 711
seq_name: gb_est1:AL157542
seq_documentation_block:
LOCUS AL157542 804 bp mRNA linear EST 24-FEB-2000
DEFINITION DKFZP761D0816.r1 761 (synonym: hamy2) Homo sapiens CDNA clone
ACCESSION AL157542
VERSION AL157542.1 GI:7057943
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
1 (bases 1 to 804)
AUTHORS
Ansorge, W., Winkner, U., Mewes, W., Well, B. and Wiemann, S.
TITLE
EST (Ansorge, W., Winkner, U., Mewes, W., Well, B. and Wiemann, S.)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Ansorge W
MIPS
Am Kiofierspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
Heidelberg, Germany) within the CDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKFZP761D0816) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
source
1..804
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZP761D0816"
/clone_lib="761 (synonym: hamy2)"
/tissue_type="amygdala"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

BASE COUNT 150 a 217 c 294 g 142 t 1 others

alignment_scores:

Quality: 943.00 Length: 193
Ratio: 4.911 Gaps: 0
Percent Similarity: 99.482 Percent Identity: 97.927

alignment block:
US-09-155-327E-9 x AL157542 ..

Align seg 1/1 to: AL157542 from: 1 to: 804

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1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
134 ATGGCAGCCCGACCGCTCGGCCAGACAGCGGCTCTGGTGGAGACTT 183
17 eValIGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
184 TGTAGGTATTAAGCTAGACAGAGGTTATGTCTGTGAGACTGAGCCCG 233
34 LysGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
234 GGGAGGGGCCAGCAGCTGACCCCTGACCAAGCCATGCGGAGCTGGA 283
51 AspGluPheGlnThrArgPheArgThrPheSerAspLeuAlaAlaG 67
284 GATGAGTTCAGACCCCTTCGCGGACCTTCTGTGATCTGGCGCTCA 333
67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
334 GCTCATGTGACCCAGGCTCAGCCCAACAGCTTCAACCCAGGCTCCG 383
84 spGluLeuPheGlnGlyLysProAsnTrpGlyArgLeuValAlaPhe 100
384 ATGAACCTTTTCAGGGGCCCAACTGGGGCCCTTGTAGCCTTCTTT 433
101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGly 117
434 GCTTTGGGGCTGCACGTGTGCGNAGAGTGTCAACAGAGATGAGAAC 483
117 OleuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGlnThrArg 134
484 ACTGGTGGACAAAGTCAGAGAGTGTATGTGTGCTACCTGAGACGGCG 533
134 eValAspTrpIleHisSerSerGlyGlyTyrPalaGluPheThrAlaLeu 150
534 TGGCTACACGAGTCCACAGACAGTGGGGCTGGGGAGTTACAGCTCA 583
151 TyrGlyAspGlyAlaLeuGlnGlnAlaArgArgLeuArgGlnGlyAsnTr 167
584 TACGGGGACGGGCC.CTGGAGAGAGCGCGGCTCTGGCGGAGGGAACTG 632
167 PalaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeu 184
633 GGCATCAGTAGAGCAGCTGTCAGCGGGGCCGCTGGCACT.GGGGCCCTGG 681
184 AlnThrValGlyAlaPhePheAlaSerLys 193
682 TAACTGAGGGGCCCTTTTGTCTAGCAAG 710

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seq_name: gb_est2:BI770566

seq_documentation_block:

LOCUS BI770566 697 bp mRNA linear EST 25-SEP-2001

DEFINITION 603060362F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5209862 5',

ACCESSION BI770566 mRNA sequence.

VERSION BI770566.1 GI:15762144

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

TITLE NIH-MGC http://mgc.nci.nih.gov/

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: rgs@frcmail.nih.gov

Tissue Procurement: Life Technologies, Inc.

FEATURES

source

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
Plate: L1A11526 row: k column: 15
High quality sequence start: 21
High quality sequence stop: 695.
Location/Qualifiers

```

1. 697
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5209862"
/clone.lib="NIH_MGC_122"
/lab_host="DH10B"
/note="Organ: pooled lung and spleen; Vector: pCMV-Sport6;
Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed and enriched for
(invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."
BASE COUNT 121 a 202 c 248 g 126 t
ORIGIN

```

alignment_scores:
Quality: 880.00 Length: 187
Ratio: 4.835 Gaps: 5
Percent Similarity: 97.326 Percent Identity: 95.722

alignment block:
US-09-155-327E-9 x BI770566 ..

Align seg 1/1 to: BI770566 from: 1 to: 697

```

1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
145 ATGGCAGCCCGACCGCTCGGCCAGACAGCGGCTCTGGTGGAGACTT 194
17 eValIGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
195 TGTAGGTATTAAGCTAGACAGAGGTTATGTCTGTGAGACTGAGCCCG 244
34 LysGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
245 GGGAGGGGCCAGCAGCTGACCCCTGACCAAGCCATGCGGAGCTGGA 294
51 AspGluPheGlnThrArgPheArgThrPheSerAspLeuAlaAlaG 67
295 GATGAGTTCAGACCCCTTCGCGGACCTTCTGTGATCTGGCGCTCA 344
67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
345 GCTTTGGGGCTGCACGTGTGCGNAGAGTGTCAACAGAGATGAGAAC 394
84 spGluLeuPheGlnGlyLysProAsnTrpGlyArgLeuValAlaPhe 100
395 ATGAACCTTTTCAGGGGCCCAACTGGGGCCCTTGTAGCCTTCTTT 444
101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGly 117
445 GCTTTGGGGCTGCACGTGTGCGNAGAGTGTCAACAGAGATGAGAAC 494
117 OleuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGlnThrArg 133
495 CACTGTGGGACAAAGTCAGAGAGTGTGAGTGTGAGTGTGAGTGTGAG 544
133 gLeuAlaAspTrpIleHisSerSerGlyGlyTyrPalaGluPheThrAla 150

```


/lab_host="DLH08", Site=1, Note: Site 2: EcoRV (destroyed); Vector: PCWV-SPORT6; Site=1: NotI; Site 2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of nonactivated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Immunogen). Research Genetics tracking code 027. Note:

```

BASE COUNT      129 a      184 c      216 g      114 t      this is a NIH-MGC library.. "
ORIGIN

alignment_scores:
    Quality:   748..50          Length:   167
              Ratio:   4.768           Gaps:     3
    Percent Similarity: 94.012       Percent Identity: 88.623

alignment_block:
US-09-155-327E-x B1910270 ..

Align seg 1/1 to: B1910270 from: 1 to: 643

1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAsph 17
|||||.....:::|||||||
140 ATGGCACCCTCCAGCGCTGCGGCCACAGCACAGGCGTGTGGTCAGACTTT 189
|||||.....:::|||||||
17 eValgIYrArGlEuAnGInLySGlTYrValCYsgIyAlAgIYPrg 34
|||||.....:::|||||||
190 TGTAGTATTAACTGATGAGCAGAAGGTTATGTCTGTGGAGCTGGCCCCG 239
|||||.....:::|||||||
34 IYgInGIYPrOAlAAlAAsPPrOleuHISglNAlAMeTAryAlAlAgly 50
|||||.....:::|||||||
240 GGGAGGGCCAGCAGCTGACCCGCTGCACCAAGCCATCGCGGAGCTTGA 289
|||||.....:::|||||||
51 AspGIuPhelGluThrArgPheArGyrThrPheSerASpLeuAlAlaGI 67
|||||.....:::|||||||
290 GATGAGTTCGAGACCGCTTCGGCCACCTTCTGTGATCTGGCGGCTCA 339
|||||.....:::|||||||
67 nLeuHISvAlThrProGlySeraLagInGlnArgPheThrGlnValSera 84
|||||.....:::|||||||
340 GGTGATGTGACCCAGGCTCAGCCCAACAAGCTTCACCCAGCTCTCG 389
|||||.....:::|||||||
84 sPgLIuPhelGInGIYPrOAsnTrpLYrArGlEuValAlAPhePhe 100
|||||.....:::|||||||
390 ATGAACCTTTTCMAAGGGGGCCCAACTGGGGCGCTTGAGCTCTTT 439
|||||.....:::|||||||
101 ValPheGlyAlAlAleuCysAlaGluSerValAsnLySGlu_MetGIuP 117
|||||.....:::|||||||
440 GTCCTGGGGCTGCACCTGTGCTGAGAGTGTCAACAAGAGCATGAGAAC 489
|||||.....:::|||||||
117 roLeuValIGlyGInValGlnAsPTripMeValAlAtYrLeuGIuThrArg 133
|||||.....:::|||||||
490 CACTGTGGGACAGAGCGAGGTGATGAGTGGCTCAGTGGAGACGG 539
|||||.....:::|||||||
134 LeuAlAsPTripLHisSerSerLYrIYrPrAlaGluPheThrAlate 150
|||||.....:::|||||||
540 CTGGCTGACTGTGATCCACAGCAGTGGGGGCTG...GAGCTGGAAAGCTAT 586
|||||.....:::|||||||
150 uTYrGLY.....AspGIyAlAleuGInGlnAlARgyArGIeuArgly 164
|||||.....:::|||||||
587 CAAGAGCTCGAGTCAGGAGATGAGAGAGAAAGCTGAGAAGCTAAAGAG 635
|||||.....:::|||||||

seq_name: gb_est2:BF785386

seq_documentation_block:
LOCUS BF785386 815 bp RNA linear EST 12-JAN-2001
DEFINITION 602111728F1 NCI CGAP_Kid14 Mus musculus cDNA clone IMAGE:4239798
VERSION 5', mRNA sequence.
ACCESSION BF785386
KEYWORDS BF785386.1 GI:12090422
SOURCE EST.
ORGANISM house mouse;
MUS musculus;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 815)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT unpublished (1999)
CONTACT Robert Strausberg, Ph.D.
```

Email: c9apbs-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1AM9853 row: h column: 07
 High quality sequence start: 3
 High quality sequence stop: 650.

FEATURES

Location/Qualifiers
 1..815

/organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4239798"
 /clone_lib="NCI CGAP Kid4"
 /lab_host="DH10B (TI phage-resistant)"
 /note="Organ: kidney; Vector: pCMV-Sport6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.75 kb. Constructed by Life
 Technologies. Note: this is a NCI-CGAP Library."

BASE COUNT 166 a 212 c 296 g 141 t

ORIGIN

alignment_scores:

Quality: 741.50 Length: 186
 Ratio: 4.119 Gaps: 1
 Percent Similarity: 96.774 Percent Identity: 91.398

alignment_block:

US-09-155-327e-9 x BF785386 ..

Align seg 1/1 to: BF785386 from: 1 to: 815

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8 ProaspthrArgAlaLeuValAlaAspPheValGlyTyrArgLeuArg1 24
  |||||||
3 CGAGACACACGGGCTCTAGTGGTACCTT.GTAGGCTTAAGCTGAGCA 51
  |||||||
24 nlysglyTyrValCysGlyAlaGlyProGlyGlyGlyProAlaAlaasp 41
  |||||||
52 GAAGGGTATGTCGTGTGGAGCTGGCCCTGGGGAAGCCCGACGCC 101
  |||||||
41 roLeuHisGlnAlaMetArgAlaAlaGlyAspGluPheGluThrArgPhe 57
  |||||||
102 CGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTT.GAGACCCGTTTC 150
  |||||||
58 ArgArgThrPheSerAspLeuAlaAlaGlnLeuHisValThrProGlyse 74
  |||||||
151 CGCCGACCTTCCTGACCTGGCCGCTACGTACACCTGACCCAGGCTC 200
  |||||||
74 rAlaGlnAlaPhePhePhePhePhePhePhePhePhePhePhePhePhe 91
  |||||||
201 AGCCACGACACGCTTCACCCAGGTTTCCGACGAACCTTTTCCAGGGGCC 250
  |||||||
91 roAsnTrpGlyArgLeuValAlaPhePheValPheGlyAlaAlaLeuCys 107
  |||||||
251 CTAACTGGGGCGCTCTGTGGCATTTCTTCTGGGGC...TCCCTGTTT 297
  |||||||
108 AlaGluSerValAsnLysGluMetGluProLeuValGlyGlnValGlnAs 124
  |||||||
298 GCTGAGAGTCTCAACAAGAAATGAGCCTTG.GTGGGACAAAGTCAGCA 346
  |||||||
124 pTyrMetValAlaTyrLeuGluThrArgLeuAlaAspTrpIleHisSer 141
  |||||||
347 TTGGATGTGGCTACCTGAGACAGACCTGTGGCTGACTGATCCACAGCA 396
  |||||||
141 erGlyGlyTrpAlaGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGlu 157
  |||||||
397 GTGGGGGCTGGGGGAGTTTCACAGCTTATACGGGAGGAGGCGCTGGAG 446
  |||||||

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158 GluAlaArgArgLeuArgGluGlyAsnTrpAlaSerValArgThrVal 174
 |||||||
 447 GAGGACACGGCT.CTCCGGAGGGGAAACGG.SCATCAGTGAAGACAGTGC 494
 |||||||
 174 uThrGlyAlaValAlaLeuGlyAlaLeuValThrValGlyAlaPhePhe 191
 |||||||
 495 GACGGGGGCGCGTGGCAGT.GGGGCGCTGTGTAACCTTGAAGGCGCTTTTGC 543
 |||||||
 191 laSerLys 193
 :::::
 544 TAGCAGCT 551

seq_name: gb_est2:BG298789

seq_documentation_block:

LOCUS BG298789 792 bp mRNA linear EST 21-FEB-2001

DEFINITION 60239657F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4511215 5',

ACCESSION BG298789

VERSION BG298789.1 GI:13063794

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: c9apbs-remail.nih.gov

Tissue Procurement: The Cepko Laboratory

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1AM10394 row: e column: 08

High quality sequence stop: 713.

Location/Qualifiers

1..792

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="IMAGE:4511215"

/clone_lib="NIH_MGC_94"

/tissue_type="retina"

/lab_host="DH10B (phage-resistant)"

/note="Organ: eye; Vector: pCMV-Sport6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 3.3 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH-MGC Library."

BASE COUNT 174 a 201 c 246 g 171 t

ORIGIN

alignment_scores:

Quality: 739.00 Length: 146

Ratio: 5.097 Gaps: 0

Percent Similarity: 99.315 Percent Identity: 98.630

alignment_block:

US-09-155-327e-9 x BG298789 ..

Align seg 1/1 to: BG298789 from: 1 to: 792

1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAsp 17

|||||
 99 ATGGCAGCCCGCAGCTCAACCCAGACACAGCGGCTCAGTGGCTGACTT 148
 |||||||
 17 eValGlyTyrArgLeuArgGlnGlyTyrValCysGlyAlaGlyProg 34
 |||||||

149 TGTAGGCTATAGCTGAGCGAGAGGCTTATGCTGTGAGCTGCCCTG 198
 34 TGTGCTGCTATAGCTGAGCGAGAGGCTTATGCTGTGAGCTGCCCTG 50
 199 GGAAGGCGCCAGCGCGAGCGCTGCTGACCAAGCGAGCGCTGCTGGA 248
 51 AAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 67
 249 GACGAGCTTGAAGACCGCTTCCGCCGACCTTCTGCTGCTGCTGCTG 297
 67 nleuhtisvalthrprogliserataglnvalphethrvalsera 84
 298 GGTACACGTCGACCGCGCTGACCGACCAACGCTTCCACCGAGCTTCCG 347
 84 spgluuephglnlglpysrvalpysrvalpysrvalpysrvalpysr 397
 348 ACNACTTTTCCAGGCGCGCTTACCTGCGCGCTTCTGCTGCTGCTT 397
 101 valphglnvalalaleucysalagluservalasnlsglmetglupr 117
 398 GCTCTTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 447
 117 oleuvalglglnvalglasprrpmetvalalafyrieuglthrargl 134
 448 TTTGGTGGGACAGCTGAGATGATGATGATGATGATGATGATGATGAT 497
 134 eualaasprpilhsersearglgltrpallglu 146
 498 TGGCTGACTGATCCACAGCATGGGGCTGGTAAGAA 535
 seq_name: gb_est1:AW258810

seq_documentation_block: 540 bp mRNA linear EST 23-DEC-1999
 LOCUS AW258810
 DEFINITION um74602.y1 Sugano mouse kidney mRna Mus musculus cDNA clone
 IMAGE:2300906 5' similar to SW:BCLM_MOUSE; P70345 APOPTOSIS
 REGULATOR BCL-W. [2] SW:BCLM_MOUSE; mRNA sequence.

ACCESSION AW258810
 VERSION AW258810.1 GI:6631791

KEYWORDS EST.
 SOURCE house mouse.

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 540)

REFERENCE

AUTHORS

Marras, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
 Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers, Y., Person
 'B', Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurr, R., Ritter
 'E', Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
 Waterston, R. and Wilson, R.

The WashU-NCI Mouse EST Project 1999

Unpublished (1999)

Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:1009678

Seq primer: custom primer used

High quality sequence stop: 465.

FEATURES

source

1..540
 /organism="Mus musculus"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone="IMAGE:2300906"
 /clone_lib="Sugano mouse kidney mRna"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"

BASE COUNT 98 a 165 c 170 g 107 t

alignment_scores:

Quality: 721.00

Ratio: 5.150

Percent Similarity: 98.592

Percent Identity: 95.775

alignment_block:

US-09-155-327E-9 x AW258810

Align seg 1/1 to: AW258810 from: 1 to: 540

1 Metalaethrproalaserthrproasprthrargalaleuvalalasp 17

|||||ATGGCGAGCCAGCCAGCTCAACCCAGACACAGCGGCTCTGAGCTGCTACTT 161

112 ATGGCGAGCCAGCCAGCTCAACCCAGACACAGCGGCTCTGAGCTGCTACTT 161

17 evalgltyrargleuarglnysgltyrvalysglalalaglprog 34

|||||TGTAGGCTATAGCTGAGCGAGAGGGGTATGCTGTGAGAGCTGGCGCTG 211

162 TGTAGGCTATAGCTGAGCGAGAGGGGTATGCTGTGAGAGCTGGCGCTG 211

34 TGTGCTGCTATAGCTGAGCGAGAGGGGTATGCTGTGAGAGCTGGCGCTG 211

117 oleuvalglglnvalglasprrpmetvalalafyrieuglthrargl 134

|||||TTTGGTGGGACAGCTGAGATGATGATGATGATGATGATGATGATGAT 497

212 GGAAGGCGCCAGCGCGAGCGCTGACCAAGCGAGCGGCTGCTGGA 261

51 AAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 67

|||||GACGAGCTTGAAGACCGCTTCCGCCGACCTTCTGACTGCGCGCTCA 311

262 GACGAGCTTGAAGACCGCTTCCGCCGACCTTCTGACTGCGCGCTCA 311

67 nleuhtisvalthrprogliserataglnvalphethrvalsera 84

|||||GCTACACGTCGACCGCGCTGACCGACCAACGCTTCCACCGAGCTTCCG 361

312 GCTACACGTCGACCGCGCTGACCGACCAACGCTTCCACCGAGCTTCCG 361

84 spgluuephglnlglpysrvalpysrvalpysrvalpysrvalpysr 100

|||||ACGAACTTTTCCAGGCGCGCTTACCTGCGCGCTTCTGCTGCTGCTT 411

362 ACGAACTTTTCCAGGCGCGCTTACCTGCGCGCTTCTGCTGCTGCTT 411

101 valphglnvalalaleucysalagluservalasnlsglmetglupr 117

|||||GCTCTTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 447

412 GCTCTTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 447

117 oleuvalglglnvalglasprrpmetvalalafyrieuglthrargl 134

|||||TTTGGTGGGACAGCTGAGATGATGATGATGATGATGATGATGATGAT 497

462 TTTGGTGGGACAGCTGAGATGATGATGATGATGATGATGATGATGAT 497

134 eualaasprpilhsersearglgltrpallglu 146

|||||TTTGGTGGGACAGCTGAGATGATGATGATGATGATGATGATGATGAT 497

512 TGGCTGACTGATCCACAGCATGGGGCTGGTAAGAA 535

seq_name: gb_est2:BT764428

seq_documentation_block:

LOCUS BT764428

DEFINITION 603050701F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5190792 5',

ACCESSION BT764428

VERSION BT764428.1 GI:15756006

KEYWORDS EST.

SOURCE human.

758 bp mRNA linear EST 25-SEP-2001

ORGANISM

Homo sapiens

REFERENCE

Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 758)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM11471 row: a column: 01
High quality sequence stop: 753.

FEATURES

source

Location/Qualifiers

1..758

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_image="5190792"

/clone_lib="NIH_MGC_116"

/lab_host="DH10B"

/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49
female, 71 yo male colon, 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH-MGC Library."

BASE COUNT

140 a 216 c 228 g 174 t

ORIGIN

alignment_scores:

Quality: 576.00 Length: 112
Ratio: 5.143 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 97.321

alignment_block:

US-09-155-327E-9 x B1764428 ..

Align seg 1/1 to: B1764428 from: 1 to: 758

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1  MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAsp 17
   |||||||
139 ATGGGAGACCCAGCTCGGCCCCAGACACAGGCGCTCTGTGGCAGACTT 188
   |||||||
17  eValGlyTyrArgLeuArgGlnGlyTyrValGlyGlyAlaGlyProG 34
   |||||||
189 TGTAGGTATTAAGCTGAGCAGCAAGGCTATGCTGTGAGAGCGTCCG 238
   |||||||
34  lYgUGlYProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
   |||||||
239 GGGAGGGCCCAAGCAGCTGACCCGCTGACCAAGCCATGCGGGAGCTGA 288
   |||||||
51  AspGluPheGluThrArgPheArgThrPheSerAspLeuAlaAla 67
   |||||||
289 GATGAGTTGAGACCCGCTCGGGCCACCTTCTGATCTGGCGGCTCA 338
   |||||||
67  nLeuHisValThrProGlySerAlaGlnAlaArgPheThrGlnValSer 84
   |||||||
339 GCTGCACTGATACCCAGGCTCAGCCCAACAGCTTACCCAGGCTCCG 388
   |||||||
84  spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhe 100
   |||||||
389 ATGAACCTTTTCAAGGGGCCCCCACTGGGGCCCGCTGTAGCTTTT 438

```

seq_name: gb_est2:BM191403

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101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsn 112
   |||||||
439 GTCCTTGGGGCTGCACCTGTCTGCTGAAGAAGTGTTC 474

```

seq_documentation_block:

LOCUS BM191403

DEFINITION daJ6a10.y1 NICHD XGC L11 Xenopus laevis cDNA clone IMAGE:5129734

5' similar to SW:ARL_XENLA 091827 APOPTOSIS REGULATOR R1, mRNA

sequence.

ACCESSION BM191403

VERSION BM191403.1 GI:17527366

KEYWORDS EST.

SOURCE African clawed frog.

ORGANISM Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

Xenopodinae; Xenopus.

1 (bases 1 to 601)

NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Martha Redbert, Steven L. Klein, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Washington University Genome Sequencing Center

clone distribution: Xenopus clones from this library are available

through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Seq primer: -40RP from G1bco

High quality sequence stop: 386.

FEATURES

source

Location/Qualifiers

1..601

/organism="Xenopus laevis"

/db_xref="taxon:8355"

/clone_image="5129754"

/clone_lib="NICHD XGC L11"

/lab_host="DH10B (phage-resistant)"

/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection (XGC
Library."

BASE COUNT

149 a 125 c 189 g 138 t

ORIGIN

alignment_scores:

Quality: 572.50 Length: 164
Ratio: 4.119 Gaps: 1
Percent Similarity: 84.756 Percent Identity: 66.463

alignment_block:

US-09-155-327E-9 x BM191403 ..

Align seg 1/1 to: BM191403 from: 1 to: 601

```

11  ArgAlaLeuValAlaAspPheValGlyTyrArgLeuArgGlnGlyTyr 27
   |||||||
119 CGGGCTTTGGTGGAGATTTTGGCGGTACAGTTATGCAACAGTAGTCT 168
   |||||||
27  rValGlyGlyAlaGlyProGlyGluGlyProAlaAlaAspProLeuHis 44
   |||||||
169 TGTIT.....CCAGACCTGCAGGACACAGCATCTGCTTTCATT 209
   |||||||
44  lAlaMetArgAlaAlaGlyAspGluPheGluThrArgPheArgThr 60
   |||||||
210 CAGCTATGGGTGCTGAGGAGATGATTTGAGAGGAGCATTCAGACAA 259

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DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: L1CM987 row: d column: 05
 High quality sequence stop: 561.
 Location/Qualifiers

FEATURES

SOURCE

1. 601
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4106836"
 /clone_lib="NIH MGC 17"
 /tissue_type="thymomyeloma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
 Site_2: XhoI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 BASE COUNT 110 a 176 c 201 g 114 t
 ORIGIN

alignment_scores:
 Quality: 558.50 Length: 147
 Ratio: 4.199 Gaps: 7
 Percent Similarity: 90.476 Percent Identity: 83.673

alignment_block:

US-09-155-327E-9 x BF204905 ..

Align seg 1/1 to: BF204905 from: 1 to: 601

4 ProAlaSerThrProAsp...ThArgAlaLeuValAlaAsp.PheValG 19
 165 CCAGCCCTGGCCGCCAGCACCGGCTGGTGCGACGACATTGTTG 214
 19 LTTATATGAGTGAAGGCGTATGCTGTGGAGCTGGCCCGGGGAG 264
 215 GTTATATGAGTGAAGGCGTATGCTGTGGAGCTGGCCCGGGGAG 264
 36 GlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGlyAspG 52
 265 GGCCGACGAGCTGACCCAGCCAGCCAGCCAGCTGGAGATGA 314
 52 upheGluThrArgPheArgArg...ThPheSerAspLeuAlaAlaGln 68
 315 GTTCGAGACCCGCTTCGGCGCTCACCCTTCTGATCTGGCGCTCAGCT 364
 69 HisVal1ThrProGlySerAlaGlnGlnArg.PheThrGlnValSerAsp 84
 365 TCATGTGATGCCAGGCTCAGCCCAACAGACTTCACCCAGTCTCCGAT 414
 85 GlnLeuPhe.GlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 101
 415 GAACTTTTGCAGAGGGGCCCACTGGGGTTCGCTTACCTCTTGG 464
 101 a1PheGlyAlaAlaLeuGlnSerValAsnGlyGlnMetGluPro 117
 465 TCTTGGGGCTGCACTGTGTGTGAGAGTGTCAACAGAGATGAGACCA 514
 118 LeuValGlyGlnValGlnAspTrpMetValAlaTrpLeuGlnThrArg 134
 515 CTGGTGGGCAAGTGCAGAGTGTGGTGTACTGTGAGAGACCGGCTCT 564
 134 uAlaAsp.TripLeuSerSerGlyGly 143
 565 GCGTGTGTGATCCAAAGAGAGTGGGT 593
 seq_name: gb_est2:BE508939

seq_documentation_block:

LOCUS BE508939 612 bp mRNA linear EST 07-AUG-2000

DEFINITION dc14h09.y1 NICHHD XGC L11 Xenopus laevis cDNA clone IMAGE:3397121 5' similar to SW:ARL_XENMLA Q91827 APOPTOSIS REGULATOR R1 ;, mRNA

ACCESSION

BE508939

VERSION

BE508939.1 GI:9728714

KEYWORDS

EST.

SOURCE

African clawed frog.

ORGANISM

Xenopus laevis

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

AUTHORS

Xenopodinae; Xenopus.

TITLE

1 (bases 1 to 612)

JOURNAL

NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

COMMENT

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

COMMENT

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.

COMMENT

Email: cgapbs-r@mail.nih.gov

COMMENT

Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.

COMMENT

cDNA Library Preparation: Life Technologies, Inc.

COMMENT

DNA Sequencing by: Washington University Genome Sequencing Center

COMMENT

Clone distribution: Xenopus clones from this library are available

COMMENT

through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov

COMMENT

Seq primer: -40RP from G1pco

COMMENT

High quality sequence stop: 439.

FEATURES

Location/Qualifiers

SOURCE

1. 612
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone="IMAGE:3397121"
 /clone_lib="NICHHD XGC L11"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: liver; Vector: pCMV-Sport6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.4 kb. Constructed by Life
 Technologies. Note: This is a Xenopus Gene Collection (XGC
) library."
 BASE COUNT 154 a 128 c 188 g 141 t 1 others
 ORIGIN

alignment_scores:
 Quality: 532.50 Length: 166
 Ratio: 3.915 Gaps: 1
 Percent Similarity: 81.928 Percent Identity: 62.651

alignment_block:

US-09-155-327E-9 x BE508939 ..

Align seg 1/1 to: BE508939 from: 1 to: 612

11 ArgAlaLeuValAlaAspPheValGlyTrpArgLeuArgGlnGlyTy 27
 121 CGGCGTTTGTGGAGGATTTTGGCGTACAAAGTTATCCCACTACTCT 170
 27 rValGlyGlyAlaGlyProGlyGlyGlyProAlaAlaAspProLeuHis 44
 171 TGT.....CCAGAGCTGCAGGACCATCTGCTTGGCAT 211
 44 lna1MetArgAlaAlaGlyAspGluPheGluThrArgPheArgArgThr 60
 212 CAGCATGCTGCTGCAGGAGATTAATTGAGGACCATTCAGCAAGCA 261
 61 PheSerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGln 77
 262 TTCACTGTGATCTCCACAGATCCAGTACCCCGGACAGCATATGC 311
 77 nArgPheThrGlnValSerAspGluLeuPheGlnGlyGlyProAsnTrp 94
 312 ACGATTCTGATAGCAGCTAGCTGTTCACAGAGGCGGTGAATTNG 361


```

|||||
1 ATGGCACCACCCGCTCAACCCACACACAGGCTCTAGTGGCTGACTT 50
17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlnValaGlyProG 34
51 TGTAGCTATTAAAGTACAGCAGAGGTTATGTCTGTGAGCTGGCCCTG 100
34 LylGlnGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
101 GGGAAAGGCCACCGCCGACCCGCTGACCAACCAATGCGGGCTGGGA 150
51 AspGluPheGluThrArgPheArgTyrPheSerAspLeuAlaAlaGly 67
151 GACGAGTTTGAAGACCCGTTCCGCCGACCTTCTGACCTGGCCGCTCA 200
67 nLeuHisValThrProGlySerAlaGlnAlaArgPheThrGlnValaSer 84
201 GCTACAGCTGACCCGACGCTCAAGCCGCAACGCTTCAACCCAGGTTCCG 250
84 SPGLuLeuPheGlnGlyLysProAsnTrpGlyArgLeuValAlaPhePhe 100
251 ACGAACTTTTCCAAAGGGGGCCCTTAACGCGGCGCTTGTGGCATTTCTT 300
101 ValPheGlyAlaAlaLeuCysAlaGlnSerValAsnLysGlnMetGluPr 117
301 GTCCTTGGGGCTGCCCTGTCTGTCTGAGAGTGTCAACAAGAAATGAGGCC 350
117 oLeuValGlyLysValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
351 TTTGGTGGGACAAAGTCAGATGATGGTGGCTTACCTGAGACACGCTG 400
134 euaAlaAspTrpIleHisSerSerGlyTyrAlaGluPheThrAlaLeu 150
401 TGGCTGATGATCCACAGCAGAGTGGGGCTGGCGGAGTTCAACCTCTA 450
151 TyrGlyAspGlyAlaLeuGlnGlnAlaArgArgLeuArgGlyAsnTr 167
451 TACGGGACCGGGCCCTGAGAGGACGCGCTGCGGAGGAGGACACTG 500
167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeu 184
501 GGCATCAGTGAAGACAGTCTCTGACGGGGCGCTGGCAGCTGGGGCCCTG 550
184 alThrValGlyAlaPhePheAlaSerLys 193
551 TAACTGTAGGGGCTTTTGTCTAGCAAG 579
seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV28333
seq_documentation_block:
ID AAV28333 standard; cDNA; 579 BP.
XX
AC AAV28333;
XX
DT 02-OCT-1998 (first entry)
XX
DE Rat bcl-y gene.
XX
KW ss: bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..579
FT /tag= a
FT /product= bcl-y
FT /note= "No stop codon given"
XX
PN US5789201-A.
XX
PD 04-AUG-1998.
XX
PF 11-FEB-1997; 97US-0798897.

```

```

XX
PR 23-FEB-1996; 96US-0012201.
XX
PR 11-FEB-1997; 97US-0798897.
XX
PA (COCE-) COGENSYS INC.
XX
PI Guastella J;
XX
DR WPI: 1998-446079/38.
XX
DR P-PSDB: AAW61391.
XX
PS
XX
CC The mammalian bcl-y genes encode a protein that is a member of the bcl-2
CC family, components in the cell death pathway. The bcl-2 family
CC have both apoptotic activity and the apoptosis blocking activity. bcl-y
CC falls in the apoptosis activity category. The recombinant protein may
CC be used to prevent uncontrolled cell growth, either by its direct
CC administration to recombinant genetic constructs to increase its
CC expression in vivo. Also, antisense constructs can be used in disorders
CC where prevention of cell death is desired.
XX
SQ Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 other:

alignment_scores:
Quality: 1002.00 Length: 193
Ratio: 5.192 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 98.964

alignment_block:
US-09-155-327E-9 x AAV28333
Align seg 1/1 to: AAV28333 from: 1 to: 579

1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
1 ATGGCACCACCCGCTCAACCCACACACAGGCTCTAGTGGCTGACTT 50
17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlnValaGlyProG 34
51 TGTAGCTATTAAAGTACAGCAGAGGTTATGTCTGTGAGCTGGCCCTG 100
34 LylGlnGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
101 GGGAAAGGCCACCGCCGACCCGCTGACCAACGCTTCAACCCAGGTTCCG 150
51 AspGluPheGluThrArgPheArgTyrPheSerAspLeuAlaAlaGly 67
151 GACGAGTTTGAAGACCCGCTTCCGGCGCACTTCTCTACCTGGCCGCTCA 200
67 nLeuHisValThrProGlySerAlaGlnAlaArgPheThrGlnValaSer 84
201 GCTACAGCTGACCCGACGCTCAAGCCGCAACGCTTCAACCCAGGTTCCG 250
84 SPGLuLeuPheGlnGlyLysProAsnTrpGlyArgLeuValAlaPhePhe 100
251 ACGAACTTTTCCAAAGGGGGCCCTTAACGCGGCGCTTGTGGCATTTCTT 300
101 ValPheGlyAlaAlaLeuCysAlaGlnSerValAsnLysGlnMetGluPr 117
301 GTCCTTGGGGCTGCCCTGTCTGTCTGAGAGTGTCAACAAGAAATGAGGCC 350
117 oLeuValGlyLysValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
351 ATGCTGGGACAAAGTCAAGATGATGGTCAACCTGAGACACGCT 400
134 euaAlaAspTrpIleHisSerSerGlyTyrAlaGluPheThrAlaLeu 150

```


XX Human bcl-w gene.
 DE
 XX
 XX Spermatoogenesis: bcl-3 gene; Bcl-2; human; fertility; infertility;
 KW animal model; ss.
 KW
 XX
 OS Homo sapiens.
 PN MO9913710-A1.
 PD 25-MAR-1999.
 PE 16-SEP-1998; 98WO-A000764.
 PR 16-SEP-1997; 97AU-0009228.
 PA (HALT-) HALT INST MEDICAL RES WALTER & ELIZA.
 PI Adams J, Cory S, Gibson L, Koentgen F, Print C;
 DR WPI: 1999-243890/20.
 DR P-PSDB; AAI05350.
 PS
 PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
 PT protein associated with Bcl-w
 XX
 PS Claim 3; Page 32; 52pp; English.
 CC The present sequence is the human bcl-w gene encoding Bcl-w protein
 CC (see AAI05350), a pro-survival member of the Bcl-2 family which is
 CC widely expressed and which is essential for spermatogenesis. The
 CC invention relates generally to a method of treatment and to an
 CC animal model for the identification of molecules and genetic
 CC sequences useful for inducing or reducing fertility of male
 CC animals. Methods are provided for inducing or reducing fertility, or
 CC for reducing fertility, by modulating spermatogenesis. An animal
 CC model carries a mutation in at least one allele of the human or
 CC murine bcl-w gene or in a gene associated with bcl-w. Such animals
 CC have disorganized seminiferous tubules and are substantially
 CC infertile, but possess no other major abnormalities as determined
 CC by histological examination. They can be used to screen for
 CC therapeutic molecules including genetic sequences capable of
 CC inducing, enhancing or otherwise facilitating spermatogenesis in
 CC animals, or which can induce infertility.
 CC
 XX
 SQ Sequence 581 BP; 104 A; 155 C; 210 G; 112 T; 0 other;

alignment_scores:
 Quality: 997.00 Length: 193
 Ratio: 5.166 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 98.446

alignment_block:

US-09-155-327e-9 x AAX25132 ..

Align seg 1/1 to: AAX25132 from: 1 to: 581

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1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspH 17
1 ATGGGACCCCAAGCCCTGGCCCAAGACACAGGGCTGTGGTGCAGACTT 50
17 eValGlyTyrArgLeuArgGlnGlyTyrValCysGlyAlaGlyProG 34
1 TGTAGGTTATTAAGCTGAGGCAAGAGGCTATGCTGTGAGCTGGCCCG 100
34 TgtGlyGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
101 GGGAGGCGCCAGCAGCTGACCCGCTGACCAAGCATTGGCGGAGCTGCA 150
51 AspGluPheGlnThrArgPheArgArgTrhPheSerAspLeuAlaAla 67
151 GATGAGTTGAGAGCCGCTTCGCGGACCTTCTGATCTGCGGCTCA 200

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67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
201 GCTGCTGTGACCCAGGCTCAGCCCAACAGCCTTCACCCAGGCTCCG 250
84 sPluLeuPheGlnGlyLysProAsnTrpGlyArgLeuValAlaPhePhe 100
251 ATGAACCTTTTCAAGGGGCGCCCAACTGGGCGCCCTTGTAGCTCTTT 300
101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluP 117
301 GTCTTTGGGCTGCACCTGTGTGAGAGAGTCTCAACAGAGATGAGAAC 350
117 OLeuValGlyLysValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
351 ACTGGTGGACAAAGTGCAGAGAGTGTGATGCTGCTTGTGAGAGAGCGGC 400
134 euAlaAspTrpIleHisSerSerGlyTyrTrpAlaGluPheThrAlaLeu 150
401 TGCTGACTGATGCACAGCAGTGGGCTGGGCGGAGTTACAGCTCTTA 450
151 TyrGlyAspGlyAlaLeuGlnGluAlaArgArgLeuArgGluLysTr 167
451 TACGGGACGGGCGCCCTGAGAGAGCGCGGCTTCTGGGAGGGAACGTG 500
167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeu 184
501 GGCATCAGTGAAGACAGTGTGACGGGCGCTGGCAGCTGGGCGCTTGG 550
184 aThrValGlyAlaPhePheAlaSerLys 193
551 TAACTGTAGGGGCTTTTGTGCTAGCAAG 579

seq_name: /SID1/gcdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV28334
seq_documentation_block:
ID AAV28334 standard; cDNA; 579 BP.
XX
XX AAV28334;
AC
XX
XX 02-OCT-1998 (first entry)
DT
XX
XX Human bcl-y gene.
DE
XX
XX ss: bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.
OS
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX CDS 1..579
XX FT /*tag= a
XX FT /product= bcl-y
XX FT /note= "No stop codon given"
XX
XX US5789201-A.
XX
XX PD 04-AUG-1998.
XX
XX PE 11-FEB-1997; 97US-0798897.
XX
XX PR 23-FEB-1996; 96US-0012201.
XX PR 11-FEB-1997; 97US-0798897.
XX
XX (COCE-) COCENSYS INC.
XX
XX PI Guastella J;
XX
XX DR WPI: 1998-446079/38.
XX DR P-PSDB; AAW61392.
XX
XX Nucleic acids encoding B-cell lymphoma-Y protein - useful for
XX PT producing recombinant protein for use in treating uncontrolled cell
XX PT growth e.g. cancers

```

XX Claim 3; Column 15/16; 27pp; English.
PS

XX The mammalian bcl-2 genes encode a protein that is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family CC family, components in the cell death pathway. The bcl-2 family CC have both apoptotic activity and the apoptosis blocking activity. bcl-2 CC be falls in the apoptosis activity category. The recombinant protein may CC be used to prevent uncontrolled cell growth, either by its direct CC administration to recombinant genetic constructs to increase its CC expression *in vivo*. Also, antisense constructs can be used in disorders CC where prevention of cell death is desired.

Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;

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alignment_scores:          length: 193
      quality:         992.00
      ratio:           5.167
Percent Similarity:        Gaps: 0
                        Percent Identity: 97.927
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alignment_block:
nc-00-155-327E-9 y AAV28334

Align seg 1/1 to: AAV28334 From: 1 to: 575

1 MetalatlnrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
1 ATGGGACCCACGAGCTGGGGCCGACACACGGGGCTTGTGGAGACTT 50
17 eValdIyTrArgLeuArgrGlnuysglYrValCysglAlaGlyProG 34
51 TGTAGCTATTAAGCTGAGGCGAAGGGTTATGCTGTGAGAGCTGGCCCCG 100
34 lYgluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaGly 50
101 GGGAGGGGCCAGCAGCTGACCTGACCCAGCCACCAACGAGGGAGCTGGA 150
51 AspGluPheGluThrArgPheArgTrpThrPheSerAspLeuAlaAlaG 67
151 GATGAGTTGAGACCCCGCTTCGGCGACCTTCGTGATCTGGCGGCTCA 200
67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
201 GCGGCACTGTGACCCGACGCTCAGGCCAACCAACGGTTTACCAGGCTCCG 250
84 spGluLeuPheGlnGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
251 ATGACCTTTTAAAGGGGGCCCAACTGGGGCCGCTTAGCCTTCTTT 300
101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGlnuGlyP 117
301 GTCCTTGGGGGCTGCACTGTGCTCAGAGTGCATCAACAGAGATGAGAAC 350
117 olauValdIyGlnValGlnAspTrpMetValAlaTyrlLeuGluThrArgL 134
351 ACTGGTGGGCAAGTGCAGAGATGATGTGTGGCTCACTGGAGACGGCGC 400
134 euAlaAspTrpIleHisSerSerGlyGlyTTPAlaGluPheThrAlaLeu 150
401 TGGCTGACTGATCCACACAGCTGGGGGCTGGCGGAGTTTACACGCTTA 450
151 TyrGlyAspGlyAlaLeuGlnGluGlnAlaArgArgLeuArgGluGlyAsnTr 167
451 TACGGGAGCGGGCCCTCGAGAGAGCGCGGGCTGTGGGGAGGGAGACTG 500
167 palAserValArgTrpValLeuThrGlyAlaValAlaLeuGlyAlaLeu 184
501 GGCATCACTGAGCAGCACTGCTGACGGGGGCGGTGGCACTGGGGGGCCCTGG 550
184 aThrValGlyAlaPhePheAlaSerLys 193
551 TTAACGTAGAAGGGCCCTTTTGTCTAGCAAG 579

```
seq_name: /SID1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AA15946
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seq_documentation_block:
  ID: AY15946 standard: cDNA: 579 BP.
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AC	AA015946;
XX	
DT	20-MAY-1999 (first entry)

AA
DE cDNA encoding the human bcl-y protein.

XX Rat bcl-y protein; Rbcl-y: human bcl-y protein; bcl-2 homologues
 KN programmed cell death; apoptosis; necrosis: cell death; stroke
 KN head trauma; Alzheimer's Disease; neutral; muscular degenerative disease;
 KN multiple sclerosis; myocardial infarction; vitally induced cell death;
 KN aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
 KN premature cell death; cell death stimulator; prolonged cell life span;
 KN kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
 KN parasitic; ss.

Homo sapiens.

PN US5883229-A.

PD 16-MAR-1999

PF 25-NOV-1997; 97US-0978523.
VY

PR	23-FEB-1996;	96US-0012201.
PR	11-FEB-1997;	97US-0798897.

PR 25-NOV-1997; 9705-0978523
XY

PA
XX
(COCE-) COCENSYS INC.

PI Guastella J;
XX

DR WPI; 1999-214150/18.
DR P-PSDB; AAW97392.

XX	Novel bcl-y homo
PT	

PT For modelling programme cost
XX

PS DISCLOSURE, CONTAINS NO INFO, ...
XX

CC The present sequence encodes human bcl-2 protein (Rbcl-y). Rbcl-y and
CC specification also describes rat bcl-2 protein thought to be involved in
CC Rbcl-y are homologues of the bcl-2 protein (Rbcl-y and Hbcl-y
CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
CC proteins may be used to treat conditions associated with a disruption of
CC the cell death pathway. If they act as cell death inhibitors, they may be
CC used in therapies to treat subjects suffering from: strokes, head trauma,
CC Alzheimer's disease, neural and muscular degenerative diseases
CC (especially multiple sclerosis), myocardial infarction, vitally induced
CC cell death, aging, spinal cord injuries and amyotrophic lateral
CC sclerosis-conditions where cells under go premature cell death as a
CC result of triggers which may or may not be apparent. They may also be
CC used in this way to develop cell lines which remain viable in culture for
CC an extended period. In contrast, if they act as cell death stimulators,
CC Rbcl-y and Hbcl-y may be used to treat conditions associated with
CC prolonged cell life span such as cancer (especially Kaposi's sarcoma and
CC lung cancer), and auto/hyperimmune diseases. They may also be used to
CC cause cell death in, and hence control, parasites.

Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;
 XX
 SQ

```

alignment_scores:      Length: 193
                        Quality: 992.00
                        Ratio: 5.167
                        Percent Similarity: 99.482
                        Percent Identity: 97.927

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alignment_block:
US-09-155-327E-9  x  AAX15946
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Align seg 1/1 to: AAX15946 from: 1 to: 579

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1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
  |||||||
1 ATGGCAGCCCAAGCTCGGCCCAACAGAGGCGCTGTGGAGAGACTT 50
  |||||||
17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
  |||||||
51 TGTAGGTATTAAGCTGAGGACAGAGGATTATGCTGTGAGCTGGCCCG 100
  |||||||
34 1yGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
  |||||||
101 GGGAGGGCCCAAGCTGAGCCACCTGACCAAGCCATGCGGGAGCTGGA 150
  |||||||
51 AspGluPheGluThrArgPheArgThrPheSerAspLeuAlaAlaGly 67
  |||||||
151 GATGAGTTGAGAGCCCGCTTCGGGACCTTCCTGATCTGCGGGCTCA 200
  |||||||
67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
  |||||||
201 GCTGCATGTGAGCCCAAGCTCAGCCCAACAGCTTCACCCAGGTCCTCG 250
  |||||||
84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
  |||||||
251 ATGAACCTTTTTCAGGGGGGCCCAACTGGGGCCCTTGTAGCCCTCTTT 300
  |||||||
101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
  |||||||
301 GTCTTTGGGGCTGCACCTGTGTGTGAGAGGTCAACAGAGATGAGAAC 350
  |||||||
117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
  |||||||
351 ACTGCTGGGAGCAAGTGCAGAGAGTGAAGTGGGCTTACTGAGACACCG 400
  |||||||
134 euAlaAspTrpIleHisSerSerGlyTyrTrpAlaGluPheThrAlaLeu 150
  |||||||
401 TGGCTGACTGATGCACAGCAGATGGGGGCTGGGGAGTTTCACAGCTCTA 450
  |||||||
151 TyrGlyAspGlyAlaLeuGlnGluAlaArgArgLeuArgGlyLysAsnTr 167
  |||||||
451 TACGGGAGACGGGGCCCTGGAGAGGCGCGCTGCGGGAGGGGAACTG 500
  |||||||
167 palAserValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuY 184
  |||||||
501 GGCATCATGTGAGAGCAGATGCTGACGGGGGCGGTCGACACTGGGGCC 550
  |||||||
184 alThrValGlyAlaPhePheAlaSerLys 193
  |||||||
551 TAACTGAGGGGCTTTTGTGTAGCAAG 579

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seq_name: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1997.DAT: AAT96577

seq_documentation_block:

ID AAT96577 standard; DNA; 583 BP.

AC AAT96577;

XX 22-APR-1998 (first entry)

XX Human bcl-2 DNA.

XX Bcl-2; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;

XX diagnosis; degenerative disease; ss.

XX Homo sapiens.

XX Key location/Qualifiers

XX CDS 1..582

XX FT /+tag a

XX FT /product= bcl-2

XX PN MO9735971-A1.

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XX PD 02-OCT-1997.
XX XX
XX PF 27-MAR-1997; 97MO-AU00139.
XX XX
XX PR 27-MAR-1996; 96AU-0008965.
XX XX
XX PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX XX
XX PI Adams JM, Cory S, Gibson LM, Holmgren SP.
XX XX
XX DR WPI: 1997-489635/45.
XX DR P-PSDB: AAW36047.
XX XX
XX PT Nucleic acid encoding apoptosis related gene bcl-2 - used to induce
XX PT or inhibit cell survival, e.g. for treatment of cancer and
XX PT degenerative diseases
XX PS
XX PS Claim 3; Page 48; 86pp; English.
XX CC
XX CC This sequence encodes a novel human gene, bcl-2, from the bcl-2 gene
XX CC family, extracted from an adult brain library. This gene promotes cell
XX CC survival, so its modulation is useful in treatment of cancer or
XX CC auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's
XX CC disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia,
XX CC human immunodeficiency virus infection or in cell transplants.
XX CC up-regulation of the gene can also be used to modify cell lines cultured
XX CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas
XX CC and to increase survival of primary explants during genetic modification.
XX CC It can be used to produce recombinant Bcl-2 for therapy, diagnosis,
XX CC antibody production or screening of potential modulators.
XX SO

```

Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;

alignment_scores:

Quality:	990.00	Length:	193
Ratio:	5.130	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	97.409

alignment_block:

US-09-155-327E-9 x AAT96577 ..

Align seg 1/1 to: AAT96577 from: 1 to: 583

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1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
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1 ATGGCAGCCCAAGCTCGGCCCAACAGAGGCGCTGTGGAGAGACTT 50
  |||||||
17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
  |||||||
51 TGTAGGTATTAAGCTGAGGACAGAGGATTATGCTGTGAGCTGGCCCG 100
  |||||||
34 1yGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
  |||||||
101 GGGAGGGCCCAAGCTGAGCCACCTGACCAAGCCATGCGGGAGCTGGA 150
  |||||||
51 AspGluPheGluThrArgPheArgThrPheSerAspLeuAlaAlaGly 67
  |||||||
151 GATGAGTTGAGAGCCCGCTTCGGGACCTTCCTGATCTGCGGGCTCA 200
  |||||||
67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
  |||||||
201 GCTGCATGTGAGCCCAAGCTCAGCCCAACAGCTTCACCCAGGTCCTCG 250
  |||||||
84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
  |||||||
251 ACGAACCTTTTTCAGGGGGGCCCAACTGGGGCCCTTGTAGCCCTCTTT 300
  |||||||
101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
  |||||||
301 CTCTTTGGGGCTGCACCTGTGTGTGAGAGGTCAACAGAGATGAGAAC 350

```

```

117 OLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
|||||
351 ACTGTGGGAGCAAGTGCAGAGTGGATGCTACTGAGACAGCGGCG 400
134 eUAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
|||||
401 TGTGTACACGATGCCACAGCAGTGGGGCTGGCGAGTTCACAGCTCTA 450
151 TyrGlyAspGlyAlaLeuGluGlnAlaArgArgLeuArgGluGlyAsnTr 167
|||||
451 TACGGGGAGCGGGCCCTGGAGAGCGCGCTGCGCGGAGGGGAACTG 500
167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGluAlaLeu 184
501 GGCATCAGTGAAGACAGTCTGACGGGGCCCTGGCAGCTGGGGCCCTGG 550
184 aThrValGlyAlaPhePheAlaSerLys 193
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551 TAACTGTAGGGGCTTTTGTCTAGCAAG 579

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seq_name: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:AAx25134

seq_documentation_block:

ID AAX25134 standard; DNA; 583 BP.

XX AAX25134;

XX 05-JUL-1999 (first entry)

XX Human bcl-w gene derivative.

XX Spermatogenesis; bcl-3 gene; bcl-2; human; fertility; infertility;

KM animal model; ss.

XX Homo sapiens.

XX W0913710-A1.

XX 25-MAR-1999.

XX 16-SEP-1998; 98WC-AU00764.

XX 16-SEP-1997; 97AU-0009228.

XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

XX Adams J, Cory S, Gibson L, Koentgen F, Print C;

XX WPI: 1999-243890/20.

XX P-PsDB; AAY05532.

XX An animal model exhibiting reduced levels of a Bcl-w protein and/or

XX protein associated with Bcl-w

XX Disclosure; Page 36; 52pp; English.

XX The present sequence is described as a derivative of the human
 CC bcl-w gene (see AAX25132) and encodes Bcl-w protein (see AAY05532), a
 CC pro-survival member of the Bcl-2 family which is widely expressed
 CC and which is essential for spermatogenesis. The invention relates
 CC generally to a method of treatment and to an animal model for the
 CC identification of molecules and genetic sequences useful for
 CC inducing or reducing fertility of male animals. Methods are
 CC provided for the treatment of infertility, or for reducing
 CC fertility, by modulating spermatogenesis. An animal model carries
 CC a mutation is at least one allele of the human or murine bcl-w gene
 CC or in a gene associated with bcl-w. Such animals have disorganised
 CC seminiferous tubules and are substantially infertile, but possess no
 CC other major abnormalities as determined by histological examination.
 CC They can be used to screen for therapeutic molecules including
 CC genetic sequences capable of inducing, enhancing or otherwise
 CC facilitating spermatogenesis in animals, or which can induce
 CC infertility.

XX Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;

alignment_scores: quality: 990.00 length: 193

Ratio: 5.130 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 97.409

alignment_block:

US-09-155-327E-9 x AAX25134 ..

Align seg 1/1 to: AAX25134 from: 1 to: 583

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1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuAlaAsp 17
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1 ATGGCCAGCCCAAGCTCGGCCCCAGACACAGCGGCTCGGGGAGACTT 50
17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
|||||
51 TGTAGGTATTAAGCTCAGCAGCAAGGTTATGTCTGTGAGCTGGCCCG 100
34 LysGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
|||||
101 GGGAGGAGCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGA 150
51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaG 67
|||||
151 GATGAGTTCAGACCCGCTTCGGGGCAGCTTCTGATCTGGCGGCTCA 200
67 pLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
|||||
201 GCTCATGTGACCCCAAGCTCAGCCAGCCAGCAAGCCTTCACCAAGTCTCCG 250
84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPheP 100
|||||
251 ACGAAGCTTTTCAAGGGGCGCCCACTGGGGCGGCTTGTAGCTTCTTT 300
101 ValPheGlyAlaAlaLeuGlyAlaGluSerValAsnLysGluMetGluPr 117
|||||
301 CTCTTTGGGCGCTGCATGTGTGCTGAGAGTGTCAACAGAGATGGAGACC 350
117 OLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
|||||
351 ACTGTGGGAGCAAGTGCAGAGTGGATGCTGCTGCTGCTGCTGCTGCTG 400
134 eUAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
|||||
401 TGTGTACACGATGCCACAGCAGTGGGGCTGGCGAGTTCACAGCTCTA 450
151 TyrGlyAspGlyAlaLeuGluGlnAlaArgArgLeuArgGluGlyAsnTr 167
|||||
451 TACGGGGAGCGGGCCCTGGAGAGCGCGCTGCGCGGAGGGGAACTG 500
167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGluAlaLeu 184
501 GGCATCAGTGAAGACAGTCTGACGGGGCCCTGGCAGCTGGGGCCCTGG 550
184 aThrValGlyAlaPhePheAlaSerLys 193
551 TAACTGTAGGGGCTTTTGTCTAGCAAG 579

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seq_name: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:AA196578

seq_documentation_block:

ID AA196578 standard; DNA; 581 BP.

XX AA196578;

XX 22-APR-1998 (first entry)

XX Mouse bcl-w DNA.

bcl-2 gene (see AAX25133) and encodes Bcl-2 protein (see AAY05533), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation in at least one allele of the human or murine bcl-2 gene or in a gene associated with bcl-2. Such animals have disorganised seminiferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility.

Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 other:

alignment_scores:
Quality: 977.00 Length: 193
Ratio: 5.142 Gaps: 0
Percent Similarity: 98.446 Percent Identity: 96.373

alignment_block:
US-09-155-327E-9 x AAX25135 ..

Align seg 1/1 to: AAX25135 from: 1 to: 581

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1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspH 17
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1 ATGCCGACCCCAAGCCCTCAACCCGACACAGCGCTCTAGTGGCTGACTT 50
17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
111 |||||
51 TGTAGGCTATAGCTGAGAGAGAGGCTTATGCTGTGAGAGCTGGGCTG 100
34 TGTAGGCTATAGCTGAGAGAGAGGCTTATGCTGTGAGAGCTGGGCTG 100
111 |||||
101 GGGAAAGCCCAAGCCCGCCGACCAAGCAAGCAAGCGGCTGCTGGA 150
34 TGTAGGCTATAGCTGAGAGAGAGGCTTATGCTGTGAGAGCTGGGCTG 100
111 |||||
51 AspGluPheGluThrArgPheArgThrPheSerAspLeuAlaAlaG 67
111 |||||
151 GACGAGTTTGAAGCCGTTTCCGCCACCTTCTGTGACCGCGGCTCA 200
67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSer 84
111 |||||
201 GCTACACGTGACCCAGGCTCAGCCAGCAAGCGCTTCAACCAGGTTCCG 250
84 spGluLeuPheGlnGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
111 |||||
251 ACACACTTTTCCAAAGGGGCCCTTAACTGGGCGCTTGTGGCATTTCTT 300
101 ValPheGlyAlaAlaLeuCysAlaGlnSerValAsnLysGluMetGluPr 117
301 GCTTTGGGGCTCCCTGTGTGTGAGAGTCAACAAAGAAATGAGACC 350
117 OLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArg 134
351 TTTGGTGGGCAAGTCCAGATTGATGCTGCTACCTGGAGACACGTC 400
134 eValAspTrpPheHisSerSerGlyTyrPheAlaGluPheThrAlaLeu 150
401 TGGCTGACTGATCCACAGCAGTGGGCGCTGGCGGACCTTCAAGCTTA 450
151 TyrGlyAspGlyAlaLeuGlnGluAlaArgArgLeuArgGlnGlySer 167
451 TACGGGACGGGGCCCTGAGAGACGACGCGCTGCGGAGGAGCAACTG 500
167 PalSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeu 184
501 GGCATGAGTACACAGTGTGACGGGGCGCTGGCAGCTGGGGCCCTTG 550

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184 aThrValGlyAlaPhePheAlaSerLys 193
111 |||||

551 TAACTGTAGGGCTTTTGTGCTACCAAG 579

seq_name: /SID51/gcdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV41925

seq_documentation_block:

ID AAV41925 standard; cDNA: 1098 BP.

AC AAV41925;

DE 20-NOV-1998 (first entry)

Nucleotide sequence of the cDNA clone Bcl-1like (HAICH29).

KW Bcl-1like (HAICH29); chronic inflammatory disease; allergic reaction;
KW Immunological disorder; autoimmune disease; anti-infectious agent; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..1098 /tag= a

FT /product= "Bcl-1like (HAICH29) protein"

XX MO9831800-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US00960.

XX 21-JAN-1997; 97US-0034205.

XX 21-JAN-1997; 97US-0034204.

XX (AUCC-) AUCCLAND UNISERVICES LTD.

PA (HDMA-) HUMAN GENOME SCI INC.

XX Feng P, Gentz RL, Krissansen GW, NI J, Rosen CA;

XX Su JY;

XX WPI: 1998-414099/35.

XX P-PSDB: AAM59884.

PS Claim 2; Fig 12A-12D; 120pp; English.

XX This is the nucleotide sequence of the cDNA clone Bcl-1like (HAICH29),
XX used in the method of the invention. The products of the clone can be
XX used for treating conditions associated with abnormal expression of
XX the polypeptides. They can be used for e.g. treating chronic
XX inflammatory diseases, immunological disorders, autoimmune diseases,
XX inflammatory diseases, various allergies, and as anti-infectious agents.
XX The products can also be used for detection and diagnosis.

XX Sequence 1098 BP; 264 A; 279 C; 325 G; 230 T; 0 other:

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Quality: 756.00 Length: 144
Ratio: 5.250 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 97.917

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101 GGGAGGCGCCAGCAGCTGACCGCGTCACACCAAGCATCGGGCAGCTGGA 150
51 AspGluPheGlnThrArgPheArgTyrThrPheSerAspLeuAlaAlaG 67
151 GATGAGTTTCAGACCCGCTTCGGGGCACCCTTCTGTGATCTGGCGCTCA 200
67 nLeuHisValThrProGlySerAlaGlnAlaArgPheThrGlnValSer 84
201 GCTGCATGTAGACCCAGGCTCAGCCCAACACAGCTTACCCAGGCTCCG 250
84 sPlGluLeuPheGlnGlyLysProAsnTrpGlyArgLeuAlaAlaPhe 100
251 ATGAACCTTTTTCAGGGGGCCCCCAACTGGGGCCGCTTGTAGCCTCTT 300
101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluP 117
301 GTCTTGGGCGCTGCACTGTGCTGAGAGTGTCAACAGAGATGGAACC 350
117 OLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArg 134
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134 euAlaAspTrpIleHisSerSerGlyTyr 144
401 TGGCTGACTGATCCACAGCAGTGGGGGCTGG 432

seq.name: /STDS1/gcgcdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV59630
seq_documentation_block:
ID AAV59630 standard; DNA; 1864 BP.
XX
AC AAV59630;
XX
DT 19-JAN-1999 (first entry)
XX
DE Human secreted protein gene 120 clone HGBG264.
XX
KW Human: secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis: cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; osteoclast; thymus;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
PN WO9839448-A2.
XX
PD 11-SEP-1998.
XX
PF 06-MAR-1998; 98WO-US04493.
XX
PR 02-OCT-1997; 97US-0061060.
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(HUMA-) HUMAN GENOME SCI INC.

WP1: 1998-506364/43.
P-PSDB: AAN74848.
Bednarik DF, Brewer LA, Carter KC, Dunn R, Ebner R, Endress GA,
Feng P, Ferlie AM, Fischer CL, Florence KA, Greene JM, Hu JS,
Kyaw H, Laffeur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA,
Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z.

P-PSDB; AAW74848.

New isolated human genes and the secreted polypeptide(s) they encoded - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders

Claim 1; Page 353-354; 721pp; English.

This sequence represents a nucleic acid molecule designated Gene 120 and from the human cDNA clone HGB2464 (deposited as clone ATCC 97902 and ATCC 209044) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAV95502) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV95911-V539812; amino acid sequences AAW74131-W57026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see AAV95911 for described uses)

sequence 1864 BP; 494 A; 403 C; 506 G; 455 T; 6 other

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alignment_scores:      length: 144
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  ratio: 5.250
  gaps: 0
Percent Similarity: 100.000 Percent Identity: 97.917
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Align seg 1/1 to: AAV59630 from: 1 to: 1864

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67  pleuHisValThnProGIySerIaGIInArpHeThrGInValSera  84
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    |||||
211  GCTGCAGTGAACCCCGAGCTCAACCCCAACAAGCCTTCACCSAGTCCG  260
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261  ATGAACCTTTTCAAGGGGGCCCCAACCTGGGGGGCCCTTGAGGCTTCTTT  310
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101  ValPheGIyAlaIaAlaIaIuCySAlaGIuSerValAsnIySGIuMetGIuPr  117
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311  GTCCTTTGGGGCTGCACGTGTGTGCTGAGAGCTGTACACAGAGAGTGAAC  360
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117  oleuValGIyGInValGIaInAspTrpMetValAlaTyRLeuGIuThrArg  134
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361  ACTGTTGGGACAACTGCAGGAGTGTGATGGTGGCCCTACCTGGAACGCGGC  410
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ID ABL32228 standard; DNA; 6049 BP.

AC ABL32228;

DT 26-MAR-2002 (first entry)

Human immune system associated gene SEQ ID NO: 201.

XX Human; immune system disease; cytosine methylation; antiastrumatic;
 KW antiarteriosclerotic; antilaminic; cytosolic; neurologic;
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
 KW antineumatic; antiastrumatic; antidiabetic; antiparasitic;
 KW antineumatic; cancer; eye disease; arteriosclerosis; anaemia;
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
 KW gene; ds.

OS Homo sapiens.

PN WO200200928-A2

03-JAN-2002
PD

02-JUL-2001; 2001WO-EP07537.

30-JUN-2000; 2000DE-1032529

XX

XX 177

[illegible]

DR WPI; 2002-130909/17.

PT Nucleic acid comprising fragment of chemically modified gene, useful

cytosine methylation

Claim 1; SEQ ID NO 201; 32pp + Sequence Listing; German.

XX The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid

CC leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention.
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alignment_scores:

Quality:	438.00	Length:	144
Ratio:	3.744	Gaps:	0
Percent Similarity:	81.250	Percent Identity:	63.889

alignment_block:

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Align seg 1/1 to: ABL32228 from: 1 to: 6049

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5051 TGTAGAGTTATAACTTACAGTACAGTACAGGATTATGTTGTGGAGTGGATTTCG 5105
34  IyGIuGIuProAlaAlaAspProLeuHisGlnAlaAlaMetArgAlaIaGlu 50
5101 GGGAGGGTTTAACTAGATGATGATGTTGTTTATTAAGTTATAGCGGTAAGTGG 5155
51  AspGluIuRheGluIuHrArgPheArgGluValThrPheSerAspLeuAlaGlu 67
5151 GATGAGAGTGCAGAGATGCTTTTGGCGGATATTTTGGATTTGATTTGGCGGTTTA 52005
67  pleuHisValThrProGluSerAlaGlnGlnAlaArgPheThrGlnValSerA 84
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seq_documentation_block

ID	standard; DNA; 1236 BP;
XY	

AC AAS00247,
XY

31-MAY-2001 (first entry)

DE Bcl-XL-DTR apoptosis-modifying fusion protein, DNA sequence.
XY

KM Huntington's disease.
KM transient ischaemic neurological injury; stroke; spinal cord injury;
KM hyper-proliferation; Alzheimer's disease; neurodegenerative disorder
KM diphtheria toxin receptor binding domain; DFR; neoplasm; tumour;
KM neuronal apoptosis; cancer; spinal muscular atrophy; ds;
KM neuronal ceroid lipofuscinosis; cancer; spinal muscular atrophy; ds;
KM Huntington's disease.

05 chimeric - Homo sapiens.
05 chimeric - Corynebacterium diphtheriae
05 chimeric - Synthetic.

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FT		/product= "Bcl-Xl-DTR fusion protein"
FT		/note= "DTR is diphtheria toxin receptor binding domain
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FT		/note= "10x Histidine tag"
FT		61..759
FT	misc_feature	/*tag= c
FT		/note= "Bcl-Xl gene from codon 1-233"
FT		760..777
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FT	misc_feature	778..1236
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FT		/note= "DTR, diphtheria toxin receptor binding domain"
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W0200112661-A2

22-FEB-2001

15-AUG-2000; 2000WO-US22293

16-AUG-1999; 99US-0149220

(HARD) HARVARD COLLEGE.
(HSC) HIS DEPT. HAYES

US DEPT HEALTH & HUMAN SERVICES

fourth, Liu X, Collier RJ,

WFL, 2001-210343/22
P-PSDB: AAM00219

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PT domains which targets protein to a cell and modifies apoptotic response

Claim 5; Page 54-56; 65pp; English

The sequence represents the coding sequence of Bcl-XL-DTR apoptosis-modifying fusion protein comprising human Bcl-XL sequence fused via a short linker to diphtheria toxin receptor binding domain (DTR). The functional apoptosis-modifying fusion protein is capable of binding a target cell and integrating into or crossing a cellular membrane of the target cell. The apoptosis-modifying fusion protein comprises at least two domains: the DTR domain, which targets the fusion protein to the target cell and the Bcl-XL domain, which modifies an apoptotic response of the target cell. The fusion protein is useful for modifying (inhibiting or enhancing) apoptosis in a target cell, such as neuron, lymphocyte, cancer, neoplasm, macrophage, epithelial, stem, tumour or hyper-proliferative cell or an adipocyte. It is also useful for reducing apoptosis in a subject after transient ischemic neuronal injury, especially spinal cord injury. The fusion protein may be used to treat various diseases and injury conditions through inhibition or enhancement of apoptotic cellular response, including neurodegenerative disorders such as Alzheimer's disease, Huntington's disease, spinal muscular atrophy, stroke episodes and unregulated cell growth as in tumours and various cancers. The apoptosis-modifying fusion protein can be delivered effectively throughout the body and targeted to selective tissue and cells.

sequence 1236 BP; 317 A; 291 C; 343 G; 285 T; 0 other,

alignment_scores:

Quality:	429.50	Length:	233
Ratio:	2.922	Gaps:	4
Percent Similarity:	63.090	Percent Identity:	39.485

alignment_block

US-09-155-327E-9 x AAS00247 ..

Align seg 1/1 to: AAS00247 from: 1 to: 1236

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seq_documentation_block:

ID AAF75960 standard: cDNA: 1742 BP.

AA75960:

22-MAY-2001 (first entry)

Rat wild-type Bcl-XL cDNA.

Rat Bcl-XL, apoptosis inhibitor; programmed cell death inhibitor;

wild-type; antiapoptotic; cell death-associated disease;

KW tissue transplant preservative; ss.

XX Rattus norvegicus.

OS WO200112807-A1.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-JP05502.

XX 17-AUG-1999; 99JP-0230642.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX Ohta S, Asoh S;

XX WPI; 2001-211219/21.

XX P-PSDB; AAB73303.

XX Modified cDNA of rat bcl-x gene and encoded protein with membrane

XX permeability to enhance uptake for effective inhibition of cell death

XX e.g. apoptosis, useful in remedies for diseases associated with cell

XX death.

XX Claim 1; Page 43-45; 56pp; Japanese.

XX The invention relates to a mutant rat Bcl-X protein and the cDNA

XX encoding it. The mutant rat Bcl-X protein (Bcl-XFNK) has the

XX substitutions Y22F, Q26W, and R165K relative to the wild-type Bcl-XL

XX protein. The invention also encompasses recombinant vectors and host

XX cells comprising the modified nucleic acid sequence. The mutant Bcl-X

XX protein is able to permeate the cell membrane, thus enhancing its

XX ability to be taken up into a cell and to act as an inhibitor of

XX apoptosis (programmed cell death). Bcl-XFNK and nucleic acids encoding

XX it are useful in remedies for diseases associated with cell death and

XX in additives for maintaining the stability of transplanted cells and

XX organs. The present sequence represents cDNA encoding wild-type rat

XX Bcl-XL.

XX Sequence 1742 BP; 377 A; 507 C; 477 G; 381 T; 0 other;

XX alignment_scores: Quality: 425.50 Length: 225

XX Ratio: 3.061 Gaps: 4

XX Percent Similarity: 61.778 Percent Identity: 40.889

XX alignment_block:

XX US-09-155-327E-9 x AAF75960 ..

XX Align seg 1/1 to: AAF75960 from: 1 to: 1742

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XX 16 AAGGACTGATCGAGATGAGAGACCCCGAGTGCATCAATGAGCAACCA 225

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DEFINITION Mus musculus Bcl-w (Bcl-w) mRNA, complete cds.
ACCESSION AF030769
VERSION AF030769.1 GI:2623249
KEYWORDS
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Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Ross, A.J., Mayhew, K.G., Moss, J.E., Parlow, A.F., Russell, L.D. and
Macgregor, G.R.
Bcl-w is required for testis homeostasis
Unpublished
2 (bases 1 to 3476)
Ross, A.J. and Macgregor, G.R.
Direct Submission
Submitted (21-OCT-1997) Center for Molecular Medicine, Emory
University, 1462 Clifton Road, Atlanta, GA 30322, USA
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BASE COUNT 796 a 814 c 991 g 875 t
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Ratio: 5.212 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.482
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17 eValGlyTyrArgLeuArgGlnLysGlyTyrValLysGlyAlaGlyProG 34
229 TGTAGGCTATTAAGCTGAGCAGAGGCTTATGCTGTGAGCTGGCCCTG 278
34 LysGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaLagL 50
279 GGAAGGCCCGACGCCCGACCGCTGACACCAAGCCATGGGGCTGCTGCA 328
51 AspGluPheGluThrArgPheArgThrPheSerAspLeuAlaAlaG1 67
329 GACGAGTTTGAACCCGTTCCCGCCACCTTCTGTGACCTGGCCGCTCA 378
67 nleuHisValThrProGlySerAlaGlnInArgPheThrGlnValSerA 84
379 GCACACAGTACACCCAGGCTCAGCCAGCAAGCTTCAACCCAGGTTCCG 428
84 speliueupheGlnGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
429 ACGAATTTTCCAAAGGGGCGCTTAACCTGGGGCGCTTGTGGCAATCTTT 478
101 ValPheGlyAlaAlaLeuGlnSerValAsnLysGluMetGluPr 117
479 GTCTTTGGGGCTGCCCTGTGTCTGAGAGTCAACAAGAAATGACGCC 528
117 oleuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
529 TTTGGTGGACCAAGTGCAGAGATTGGATGTGGCTTACCTGAGACAGCTC 578
134 euAlaAspTrpIleHisSerSerGlyGlyTyrPalagluPheThrAlaLeu 150
579 TGGCTGACTGATCCACAGCAGTGGGGGCTGGCGGAGTCTACAGCTCTA 628

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151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
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seq_name: gb_pat:AR020779

seq_documentation_block: 579 bp DNA linear PAT 05-DEC-1998
 LOCUS AR020779
 DEFINITION Sequence 1 from patent US 5789201.
 ACCESSION AR020779
 VERSION AR020779.1 GI:3975394

KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE
 1 (bases 1 to 579)
 AUTHORS Guastella,J.
 TITLE Genes coding for bcl-1 and bcl-2 homologue
 JOURNAL Patent: US 5789201-A 1 04-AUG-1998;
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BASE COUNT 111 a 157 c 198 g 113 t
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 Ratio: 5.192 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 98.964

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seq_documentation_block: 582 bp mRNA linear ROD 28-FEB-2000
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 DEFINITION Rattus norvegicus Bcl-w (bcl-w) mRNA, complete cds.
 ACCESSION AF096291
 VERSION AF096291.1 GI:3747129

KEYWORDS
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE
 1 (bases 1 to 582)
 AUTHORS Hamner,S., Skoglusa,Y. and Lindholm,D.
 TITLE Differential expression of bcl-1 and bcl-2 messenger RNA in the
 JOURNAL Neurosci 91 (2), 673-684 (1999)
 MEDLINE 99292146
 PUBMED 10366024

REFERENCE
 2 (bases 1 to 582)
 AUTHORS Hamner,S., Skoglusa,Y. and Lindholm,D.
 TITLE Direct Submision
 JOURNAL Submitted (01-OCT-1998) Developmental Neuroscience, Uppsala
 University, Box 587, BMC, Uppsala 751 23, Sweden
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 Location/Qualifiers

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BASE COUNT 111 a 157 c 200 g 114 t
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 Quality: 1002.00 Length: 193
 Ratio: 5.192 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 98.964

alignment_block:

US-09-155-327e-9 x AF096291

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seq_documentation_block:
LOCUS      HSU59747                582 bp      mRNA      linear      PRI 29-SEP-1996
DEFINITION Human Bcl-2 (bcl-2) mRNA, complete cds.
ACCESSION  U59747
VERSION    U59747.1  GI:1572492
KEYWORDS
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 582)
AUTHORS   Gibson,L., Holmgreen,S.P., Huang,D.C., Bernard,O., Copeland,N.G.,
            Jenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S.
            bcl-2, a novel member of the bcl-2 family, promotes cell survival
            Oncogene 13 (4), 665-675 (1996)
TITLE     JOURNAL MEDLINE
REFERENCE 2 (bases 1 to 582)

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AUTHORS Gibson,L., Holmgreen,S.P., Huang,D.C.S., Bernard,O., Adams,J.M. and Cory,S.
 TITLE Direct Submission
 JOURNAL Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia

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gene
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BASE COUNT 104 a 156 c 211 g 111 t
 ORIGIN

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 Ratio: 5.166 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 98.446

alignment_block:

US-09-155-327e-9 x HSU59747

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201 GCTACACGTGACCCAGCGCTCAGCCAGCAGCAGCTTCAACCAGCTTCCG 250
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seq_name: gb-pr:BC021198

seq_documentation_block:

LOCUS BC021198 1437 bp mRNA linear PRI 22-JAN-2002
 DEFINITION Homo sapiens, BCL2-like 2, clone MGC:10675 IMAGE:3944307, mRNA,
 complete cds.

ACCESSION BC021198 GI:18203706

VERSION BC021198.1

KEYWORDS MGC.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1437)

AUTHORS Strausberg, R.

JOURNAL Direct Submission
 Submitted (14-JAN-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov

COMMENT Contact: MGC help desk
 Email: cgaps-remail.nih.gov
 Tissue Procurement: DCTD/DRP
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: http://www.nisc.nih.gov/
 Contact: nisc.mgc@nih.gov

Contact: nisc.mgc@nih.gov
 Shevchenko, Y., Wetherby, R.D., Beckstrom-Sternberg, S.M.,
 Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
 Lim, M., Maduro, O.L., Masello, C., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Snyder, B., Stantipop, S., Thomas, P.J.,
 Tjongson, E.E., Touchman, J.W., Tsurgou, C., Vogt, J.L., Walker, M.A.,
 Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Series: IRAL Plate: 15 Row: k Column: 19
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 14574571.

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 Ratio: 5.166 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 98.446

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67 nLeuHisValThrProGlySerAlaGlnArgPheThrGlnValSerA 84
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seq_name: gb-pr:D87461

seq_documentation_block:

LOCUS D87461 3542 bp mRNA linear PRI 06-OCT-2001
 DEFINITION Human mRNA for KIAA0271 gene, complete cds.
 ACCESSION D87461
 VERSION D87461.1 GI:1944417

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seq_documentation_block:
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DEFINITION Sequence 6 from Patent EP0932674.
ACCESSION AX022529
VERSION AX022529.1 GI:10046125
KEYWORDS
SOURCE
ORGANISM
unidentified.
unclassified.
REFERENCE
1 (bases 1 to 583)
AUTHORS Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.
TITLE A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
apoptosis-controlling genes
JOURNAL Patent: EP 0932674-A 6 04-AUG-1999;
AMRAD OPERATIONS PTY LTD (AU)
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BASE COUNT 105 a 157 c 210 g 111 t
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Ratio: 5.130 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 97.409
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201 GCTGATGTGACCCAGCCTCAGCCACACAGCCTTACCCAGGCTCCG 250
84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
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251 ACGAACTTTTCAAGGGGGCCCACTGGGGCCGCTTGAGCTTCTTT 300
101 ValPheGlyAlaAlaLeuGlyAlaGlySerValAsnLysGluMetGluPr 117
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301 CTCTTTGGGGCTGCATGCTGTGCTGAGAGTGTCAACAGAGATGGAACC 350
117 OleuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
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351 ACTGGTGACAGAGTGCAGAGTGTGATGTGCTTACCTGAGACGGCGC 400
134 euaAlaAspTrpLeuHisSerSerGlyGlyTyrAlaGluPheThrAlaLeu 150
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401 TGGCTGACTGATCCACAGCAGTGGGGCTGGCGGAGTTCAACAGCTCTA 450
151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
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451 TACGGGAGACGGGGCCCTGGAGAGCGCGGCTGCGGGAGGGAACTG 500
167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
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501 GGCATGAGTGAAGACAGTCTACGCGGGGCGCTGCGACCTGGCGCCCTG 550
184 alThrValGlyAlaPhePheAlaSerLys 193
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551 TAACTGTAGGGGCTTTTGTCTAGCAAG 579
seq_name: gb_pat:AX030817

seq_documentation_block:
LOCUS AX030817 583 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 6 from Patent WO9735971.
ACCESSION AX030817
VERSION AX030817.1 GI:10278311
KEYWORDS
SOURCE
ORGANISM
unidentified.
unclassified.
REFERENCE
1 (bases 1 to 583)
AUTHORS Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.
TITLE A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
apoptosis-controlling genes

```

JOURNAL

Patent: WO 9735971-A 6 02-OCT-1997;
ADAMS JERRY MCKEE (AU) ; HOLMGREEN SHAUN P (AU) ; CORY SUZANNE (AU)

FEATURES

; GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)
Location/Qualifiers

source

1..583
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/db_xref="taxon:32644"
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BASE COUNT 105 a 157 c 210 g 111 t
ORIGIN

alignment_scores:

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Ratio: 5.130 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 97.409

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US-09-155-327E-9 x AX030817 ..

Align seg 1/1 to: AX030817 from: 1 to: 583

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1  MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAsp 17
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17 eValGlyTyrArgLeuArgGlnysGlyTyrValCysGlyAlaGlyProG 34
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51 TGTAGGTTATAGCTGAGGCGAAGGGTTATGTCGTGGAGCTGGCCCG 100
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34 1yGlnGlyProAlaAlaAspProLeuHISGlnAlaMetArgAlaAlaGly 50
  |||||||
101 GGGAGGGCCCGACGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTTGA 150
  |||||||
51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaG 67
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151 GAGGAGTTGAGAGCCCGCTCCGGCGCACTTCTGTGATCGGGCGCTCA 200
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67 nLeuHISValThrProGlySerAlaGlnAlaArgPheThrGlnValSera 84
  |||||||
201 GCTGCATGTGACCCAGGCTCAGCCCAACGCTTCAACCCAGGCTCTCG 250
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101 ValPheGlyAlaAlaLeuCysAlaGluSerValAlaGlnysGluMetGluP 117
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501 GGCATCTGATGAGGACAGTCTGACGGGGCCGCTGGCACTGGGGCCCTGG 550

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184 alThrValGlyAlaPhePheAlaSerLys 193
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551 TAACTGAGGGCCCTTTTGTCTAGCAAG 579

seq_name: gb_pat:AX022531

seq_documentation_block:

LOCUS AX022531 581 bp DNA linear PAT 07-SEP-2000

DEFINITION Sequence 8 from Patent EP0932674.

ACCESSION AX022531

VERSION AX022531.1

KEYWORDS GI:10046127

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

CDS

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BASE COUNT 105 a 164 c 195 g 117 t
ORIGIN

alignment_scores:

Quality: 977.00 Length: 193
Ratio: 5.142 Gaps: 0
Percent Similarity: 98.446 Percent Identity: 96.373

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US-09-155-327E-9 x AX022531 ..

Align seg 1/1 to: AX022531 from: 1 to: 581

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17 eValGlyTyrArgLeuArgGlnysGlyTyrValCysGlyAlaGlyProG 34
  |||||||
51 TGTAGGTTATAGCTGAGGCGAAGGGTTATGTCGTGGAGCTGGCCCG 100
  |||||||
34 1yGlnGlyProAlaAlaAspProLeuHISGlnAlaMetArgAlaAlaGly 50
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101 GGGAGGGCCCGACGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTTGA 150
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51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaG 67
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67 nLeuHISValThrProGlySerAlaGlnAlaArgPheThrGlnValSera 84
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84 sPGLuLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
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101 ValPheGlyAlaIleuCysAlaGluSerValAsnLysGluMetGluPr 117
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 301 GTCTTTGGGGCTGCCCTGTGCTGCTGAGAGTGTACAAAGAAATGGAGCC 350
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 351 TTTGGTGGGACAAAGTCCAGATGTGATCGTGCTACCTGGAGACAGTTC 400
 134 euaAlaAspTrpIleHisSerSerGlyTyrTPAlaGluPheThrAlaLeu 150
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 151 TyrGlyAspGlyAlaLeuGluGlnAlaArgArgLeuArgGluGlyAsnTr 167
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 451 TACGGGAGCGGGGCGCTGGAGAGCACGCGCTCGCGGAGGCAACTG 500
 167 palAspValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeu 184
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 551 TAACCTAGGGCGCTTTTGTGTACCAAG 579

seq_name: gb_pat:AX030819

seq_documentation_block:

LOCUS AX030819 581 bp DNA linear PAT 20-SEP-2000
 DEFINITION Sequence 8 from Patent WO9735971.
 ACCESSION AX030819
 VERSION AX030819.1 GI:10278313

KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE

JOURNAL
 1 (bases 1 to 581)
 Adams,J.M., Holmgren,S.P., Cory,S. and Gibson,L.M.
 A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
 apoptosis-controlling genes
 Patent: WO 9735971-A 8 02-OCT-1997;
 ADAMS JERRY MCKEE (AU) ; HOLMGREN SHAUN P (AU) ; CORY SUZANNE (AU)
 ; GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)
 Location/Qualifiers

FEATURES
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CDS

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 RLREGNMA"

BASE COUNT 105 a 164 c 195 g 117 t
 ORIGIN

alignment_scores:
 Quality: 977.00 Length: 193
 Ratio: 5.142 Gaps: 0
 Percent Similarity: 98.446 Percent Identity: 96.373

alignment_block:

US-09-155-327E-9 x AX030819 ..
 Align seg 1/1 to: AX030819 from: 1 to: 581

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seq_documentation_block:

LOCUS CNS00008 196292 bp DNA linear PRI 22-MAY-2001
 DEFINITION Human chromosome 14 DNA sequence BAC R-124D2 of library RpCt-11
 from chromosome 14 of Homo sapiens (Human), complete sequence.

ACCESSION AL049829
 VERSION AL049829.4 GI:8217859
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 1 (bases 1 to 196292)
 Mammalia: Euteria: Primates: Catarrhini: Hominiidae: Homo.
 Heilig,R., Petrij,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,
 Brothier,P., Catillo,L., Barde,V., Pelletier,E., Attienave,F.,
 Levy,M., Eckenberg,R., Bruns,T., deBerardinis,V., Cruaud,C.,
 Gyapay,G., Saurin,W. and Weissbach,J.
 Gyapay,G., Saurin,W. and Weissbach,J.
 Sequencing of the human chromosome 14
 Unpublished
 2 (bases 1 to 196292)
 Genoscope.
 Direct Submission
 Submitted (21-MAY-2001) Genoscope - Centre National de Sequencage ;
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 On Jun 3, 2000 this sequence version replaced gi:6138746.
 ----- Genoscope Center
 Center: Genoscope / Centre National de Sequencage

17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
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 51 TGTAGGCTATAGGCTGAGAGGAGGTTATGTCTGTGGAGTGGGCGCTG 100
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 151 GACGAGTTTGAGACCGTTTCCGCGGACCTTCTCTACTGCGCGCTCA 200
 67 nLeuHisValThrProGlySerAlaGlnAlaArgPheThrGlnValSera 84
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 301 GTCTTTGGGGCTGCCCTGTGCTGCTGAGTGTCAACAAGAAATGGAGCC 350
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 351 TTTGGTGGGACAAAGTCCAGATGTGATGTGCTGCTACCTGGAGACAGCTC 400
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 184 alThrValGlyAlaPhePheAlaSerLys 193
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 551 TAACCTAGGGCGCTTTTGTGTACCAAG 579

Center code: GS
Web site: <http://www.genoscope.cns.fr/>
Contact: SeqRef@genoscope.cns.fr

The following BAC sequence is oriented from the T7 to the SP6 end.
Upstream BAC (overlapping the T7 end) : R-244E17
Downstream BAC (overlapping the SP6 end) : C-2201G16 (AC-AL132855)

Summary Statistics
Assembly Program: Phrap; Version 2.0

Quality coverage: 7.94x in Q20 bases; sum-of-contigs

Overall quality chart :

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Range      : bases
1 - 9      :
10 - 19    :
20 - 29    : 10
30 - 39    : 30
40 - 49    : 829
50 - 59    : 1909
60 - 69    : 5193
70 - 79    : 18093
80 - 89    : 58972
90 - 99    : 111256

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Percentage of bases with a quality value >= 40 : 99 %.

Location/Qualifiers

1. 196292

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/db_xref="taxon:9606"

/chromosome="14"

/clone="R-124D2"

/clone_11b="R-PCR-11"

/note="matching EMBL:AA908790"

RHdb:RH102162

dbSTS:STS69699

Identified using the e-PCR software (G. Schuler)"

80433. 80566

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RHdb:RH98727

dbSTS:STS68485

Identified using the e-PCR software (G. Schuler)"

82164. 82299

/note="matching EMBL:H79035"

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Identified using the e-PCR software (G. Schuler)"

93580. 93808

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Identified using the e-PCR software (G. Schuler)"

107758. 107951

/note="matching EMBL:R94929"

RHdb:RH65111

dbSTS:STS45044

Identified using the e-PCR software (G. Schuler)"

107996. 108181

/note="matching EMBL:D11677"

RHdb:RH47139

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Identified using the e-PCR software (G. Schuler)"

138462. 138738

/note="matching EMBL:R59134"

RHdb:RH53972

dbSTS:STS42930

Identified using the e-PCR software (G. Schuler)"

138509. 138658

/note="matching EMBL:M78864"

RHdb:RH95543

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dbSTS:STS24710

Identified using the e-PCR software (G. Schuler)"

138568. 138647

/note="matching EMBL:M78986"

RHdb:RH28416

dbSTS:STS20162

Identified using the e-PCR software (G. Schuler)"

138568. 138677

/note="matching EMBL:M78946"

RHdb:RH28671

dbSTS:STS20163

Identified using the e-PCR software (G. Schuler)"

138805. 138926

/note="matching EMBL:H72023"

RHdb:RH68657

dbSTS:STS48564

Identified using the e-PCR software (G. Schuler)"

161617. 161761

/note="matching EMBL:AA452257"

RHdb:RH92419

dbSTS:STS65422

Identified using the e-PCR software (G. Schuler)"

194804. 194903

/note="matching EMBL:N91549"

RHdb:RH76320

dbSTS:STS53407

Identified using the e-PCR software (G. Schuler)"

50870 a 45673 c 47123 g 52626 t

BASE COUNT

ORIGIN

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Quality: 863.50 Length: 399

Ratio: 4.474 Gaps: 2

Percent Similarity: 48.371 Percent Identity: 47.118

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US-09-155-327E-9 x CNS00008 ..

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89826 ATGGCAGCCCGACGCTCGGCGCCACACACACGCTGCGGCGACTT 89875

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89876 TGTAGGTATTAAGCTGAGCAGAGAGGTTATGTCTGTGAGACTG6CCCCG 89925

34 lYcGlnGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaGly 50

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51 AspGluPheGluThrArgPheArgThrPheSerAspLeuAlaAlaG 67

89976 GATGAGTTGAGACCCGCTTCGCGGCGACCTTCTGATCTGCGGCTCA 90025

67 nLeuHisValThrProGlySerAlaGlnArgPheThrGlnValSerA 84

90026 GCTGATGTGAGCCCGACGCTGACCAAGCGCTTCACCCAGGTCTCG 90075

84 sPGluLeuPheGlnGlyProAsnTrpGlyArgLeuValAlaPhePhe 100

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 117 oleuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
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 162 euArgGluGlyAsnTrpAlaSerValArgThrValLeuThrGlyAlaVal 178
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 179 AlaLeuGlyAlaLeuValThrValGlyAlaPheAlaSerLys 193
 90976 GCACCTGGGGGCGCTGTACTGTAAGGGCGCTTTTGTAGCAAG 91020

seq_name: gb.AC079885

seq_documentation_block:

LOCUS AC079885 151212 bp DNA linear HTG 08-NOV-2000

DEFINITION Rattus norvegicus chromosome 4 clone RP31-246H8 strain Brown

ACCESSION AC079885.2 GI:11120768

VERSION AC079885.2

KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.

SOURCE Norway rat.

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus

1 (bases 1 to 151212)

Beckstrom,Sternberg,S.M., Benjamin,B., Blakesley,R.W.,

Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Gupta,J.,

Ho,S.-L., Idol,J., Karlins,E., Lee-Hin,S.-Q., Legaspi,R., Lim,M.,

Maduro,O.L., Maduro,V.B., Mastrian,S.D., McCloskey,J.C.,

McDowell,J., Pearson,R., Prasad,A., Snyder,B., Stantipop,S.,

Thomas,J.W., Thomas,P.J., Tjongson,E.E., Touchman,J.W.,

Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D. and Green,E.D.

Unpublished

2 (bases 1 to 151212)

Direct Submission

Submitted (16-SEP-2000) NIH Intramural Sequencing Center, 8717

Groveomont Circle, Gaithersburg, MD 20877, USA

On Nov 8, 2000 this sequence version replaced gi.10179358.

----- Genome Center

Center: NIH Intramural Sequencing Center

Center code: NISC

Web site: http://www.nisc.nih.gov

Contact: nisc.mouse@nih.gov

----- Project Information

Center project name: rk

Center clone name: 246H8

----- Summary Statistics

Sequencing vector: plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 147800 bases at least Q40

Consensus quality: 149333 bases at least Q20

Insert size: 145000; agarose-fp
 Quality coverage: 11.76x in Q20 bases; sum-of-contigs
 Quality coverage: 11.30x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently
 consists of 5 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved

1 20440: contig of 20440 bp in length
 * 20441 20540: gap of unknown length
 * 20541 41009: contig of 20469 bp in length
 * 41010 41109: gap of unknown length
 * 41110 65552: contig of 24443 bp in length
 * 65553 65653: gap of unknown length
 * 65653 110365: contig of 44713 bp in length
 * 110366 110465: gap of unknown length
 * 110466 151212: contig of 40747 bp in length.

FEATURES

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                   clone_end:T7
                   vector_side:left"
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ORIGIN

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ACCESSION  AC084240
VERSION    AC084240.1 GI:10864175
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SOURCE     Norway rat.
ORGANISM   Rattus norvegicus
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
1 (bases 1 to 181282)
Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W.,
Bouffard, G.G., Brinkley, C., Dietrich, N.L., Gupta, J., Ho, S.-L.,
Idol, J., Lee-Lin, S.-O., Legaspi, R., Lim, M., Maduro, Q.L.,
Maduro, V.B., Mastrian, S.D., McCloskey, J.C., McDowell, J.,
Pearson, R., Prasad, A., Snyder, B., Stantipop, S., Thomas, J.W.,
Thomas, P.J., Tjongson, E.E., Touchman, J.W., Tyan, J.T., Tsurgon, C.,
Vogt, J.L., Walker, M.A., Weherby, K.D. and Green, E.D.
NISC Mouse Sequencing Initiative
Unpublished
2 (bases 1 to 181282)
Green, E.D.
Direct Submission
Submitted (18-OCT-2000) NIH Intramural Sequencing Center, 8717
Groveomont Circle, Gaithersburg, MD 20877, USA
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc.mouse@nih.gov
----- Project Information
Center project name: r1
Center clone name: 103121
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 179798 bases at least Q40
Consensus quality: 180132 bases at least Q30
Consensus quality: 180274 bases at least Q20
Insert size: 138000; agarose-fp
Insert size: 160000; pulse-field-gel
Insert size: 180982; sum-of-contigs
Quality coverage: 15.02x in Q20 bases; agarose-fp
Quality coverage: 12.95x in Q20 bases; pulse-field-gel
Quality coverage: 11.45x in Q20 bases; sum-of-contigs

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* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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1      5430: contig of 5430 bp in length
*      5531: gap of unknown length
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Location/Qualifiers

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Thu Jun 6 16:39:21 2002

us-09-155-327e-7.p2n.rml

Page 1

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Date: Jun 6, 2002 2:32 PM
About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

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Patent No. 5789201
GENERAL INFORMATION:
APPLICANT: Gustella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140001
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
US-08-798-897-2

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; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483, 0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 579 base pairs
;
; TYPE: nucleic acid
;
; STRANDEDNESS: both
;
; TOPOLOGY: both
;
; MOLECULE TYPE: cDNA
;
; US-08-978-523-2

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  Quality: 1002.00      Length: 193
  Ratio: 5.219          Gaps: 0
  Percent Similarity: 99.482  Percent Identity: 99.482

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51 TGTAGGTATTAAGCTGAGGAGCAAGAGGTATGTCTGTGAGCTGGCCCG 100
34 LysGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
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101 GGGAGGGCCCGACAGCTGACCCAGCCAGTGCACCAAGCCATGGGGCAGTGA 150
51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaG 67
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151 GATGAGTTGAGACCCGCTTCGGCCGACCTTCTGATCTGGGGCTCA 200
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201 GGTGAGATGTGACCCCGAGCTCAGCCCAACAGAGCTTACCCAGGCTCCG 250
84 spGUleuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
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seq_documentation_block:
; Sequence 1, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John

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TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
 TITLE OF INVENTION: Homologue
 NUMBER OF SEQUENCES: 53
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 STREET: 1100 New York Avenue, N.W., Suite 600
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/798,897
 FILING DATE: February 11, 1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Esmond, Robert W.
 REGISTRATION NUMBER: 32,893
 REFERENCE/DOCKET NUMBER: 1483.0140001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2540
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 579 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 MOLECULE TYPE: cDNA
 US-08-798-897-1

alignment_scores:
 Quality: 996.00 Length: 193
 Ratio: 5.161 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 98.446

alignment_block:
 US-09-155-327e-7 x US-08-798-897-1 ..

Align seg 1/1 to: US-08-798-897-1 from: 1 to: 579

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|||||
51 TGTAGGCTATAGCTGAGACAGAAAGGTTATGCTGTGAGAGCTGGCCCTG 100
34 yGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
|||||
101 GGGAGGCGCCAGCAGCCGACCCGCTGCACCAACCAATGGGGGAGCTGGA 150
51 AspGluPheGluThrArgPheArgGlyThrPheSerAspLeuAlaGlu 67
|||||
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seq_name: /cgn2_6/ptodata/1/lna/5B_COMB.seq:US-08-978-523-1

seq_documentation_block:
 Sequence 1, Application US/08978523

Patent No. 5883229

GENERAL INFORMATION:

APPLICANT: Guastella, John

TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/978,523

FILING DATE: herewith

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/798,897

FILING DATE: February 11, 1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 1483.0140002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2500

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 579 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: cDNA

US-08-978-523-1

alignment_scores:
 Quality: 996.00 Length: 193
 Ratio: 5.161 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 98.446

alignment_block:

US-09-155-327E-7 x US-08-978-523-1 ..

Align seg 1/1 to: US-08-978-523-1 from: 1 to: 579

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1 ATGGGAGCCCGCCAGCTCAACCCAGACACACGGGCTCTAGTGGCTGACT 50
17 eValGlyTyrLeuArgGlnGlyTyrValCysGlyAlaGlyProG 34
51 TTAGGCTATTAAGCTGACACAGAGGTTATGTCTGTGGAGCTGGCCCTG 100
34 LyGlnGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaGly 50
101 GGGAGAGCCCGACGACGCCAGCCGCTGCACCAAGCCATCGGGGACCTGA 150
51 AspGluPheGlnThrArgPheArgTrpPheSerAspLeuAlaAlaG 67
151 GAGAGCTTTGAGACCCGCTCCGGGCGACCTTCTCTGACCTGGCCGCTCA 200
67 MetHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSer 84
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151 TyrGlnAspGlyAlaLeuGlnGlnAlaArgArgLeuArgGlnGlyAsnTr 167
451 TACGGGAGCGGGCCCTGAGAGAGGACAGCGGCTGCGGAGGGGAACTG 500
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184 alThrValGlyAlaPhePheAlaSerLys 193
551 TAACTGAGGGGCTTTTGTGTCAGCAAG 579

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seq_name: /cgn2/6/ptodata/1/1na/5A_COMB.seq:US-08-081-448-5

seq_documentation_block:

Sequence 5, Application US/08081448

Patent No. 5646008

GENERAL INFORMATION:

APPLICANT: Thompson, Craig B.

APPLICANT: Boise, Lawrence H.

TITLE OF INVENTION: Vertebrate Apoptosis Gene:

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Arnold, White & Durkee

STREET: 321 No. 5646008th Clark Street, Suite 800

CITY: Chicago

STATE: IL

COUNTRY: USA

ZIP: 60610

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/081,448
FILING DATE: 19930622
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646008thrup, Thomas E.
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-744-0090
TELEFAX: 312-755-4489
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 135..836
US-08-081-448-5

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alignment_scores:

Quality: 428.50 Length: 224
 Ratio: 3.018 Gaps: 4
 Percent Similarity: 63.393 Percent Identity: 40.625

alignment_block:

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Align seg 1/1 to: US-08-081-448-5 from: 1 to: 926

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28 .....
250 AAGGAGTGAATGGAGATGGAGACCCCACTGCTCATATGCAACCA 299
34 .....GlyGlnGlyProAlaAlaAsp..... 40
300 TCCTGGACCTGGCAGACAGCCCGGCTGATGAGGACACTGCCACAG 349
41 .....ProLeuHisGlnA 45
350 CACCACTTTGATGCCCGGAGCTGATCCCATGGCAGACAGTAAAGAG 399
45 lAmetArgAlaAlaGlyAspGluPheGlnThrArgPheArgTrpPhe 61
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62 SerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGln 78
450 AGTGACCTGACATCCAGCTCCACATCCACCCAGGAGCAGCATATCAGAG 499
78 gPheThrGlnValSerAspGluLeuPheGlnGlyGlyProAsnTrpGly 95
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650 TTACCGATGACACACCTGACCTTGATCCAGAGAACGCGCGTGG 699
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; Patent No. 5834309
; Patent No. 5834309 5710045
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.
; APPLICANT: Boise, Lawrence H.
; TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,670A
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,448
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARCD:090--1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..836
; US-08-470-670A-6

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alignment_scores:
Quality: 428.50
Ratio: 3.018

Length: 224
Gaps: 4

Percent Similarity: 63.393 Percent Identity: 40.625
align_block:
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seq_documentation_block:
; Sequence 1, Application US/08481739
; Patent No. 6143291
; GENERAL INFORMATION:
; APPLICANT: June, Carl H. and Thompson, Craig B.
; TITLE OF INVENTION: METHODS FOR ENHANCING T CELL SURVIVAL
; TITLE OF INVENTION: BY AUGMENTING BCL-XL PROTEIN LEVELS
; NUMBER OF SEQUENCES: 4

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Page 6

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seq_documentation_block:
? Sequence 1, Application US/09167921A
? Patent No. 6172216
? GENERAL INFORMATION:
? APPLICANT: Bennett, C. Frank
? APPLICANT: Dean, Nicholas M.
? APPLICANT: Monia, Brett P.
? APPLICANT: Nickoloff, Brian J.
? APPLICANT: Zhang, Qinqiong
? TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
? FILE REFERENCE: ISPH-0324
? CURRENT APPLICATION NUMBER: US/09/167, 921A
? CURRENT FILING DATE: 1998-10-07
? NUMBER OF SEQ. IDS: 50

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?      LOCATION: (135)..(836)
?      PUBLICATION INFORMATION:
?      DATABASE ACCESSION NUMBER: L20121 Genbank
?      DATABASE ENTRY DATE: 1994-07-26
US-09-167-921-1

alignment_scores:
    Quality:   428.50          Length:   224
    Ratio:     3.018           Gaps:       4
Percent Similarity: 63.393    Percent Identity: 40.625

alignment_block:
US-09-155-327E-7 x US-09-167-921-1      ..
Align seg 1/1   to: US-09-167-921-1   from: 1   to: 926

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34 .....GlyGluGlyProAlaAlaAsp..... 40
300 TCCTGGACCTGGCAGACAGCCCGGCTGATGAGCCACCTGCCAGAG 349
41 .....ProLeuHisGlnA 45
350 CAGCAGTTTGGATGCCGGGAGGTGATCCCATGCGACGAGTAAACGAG 399
45 lametargAlaAlaGlyAspGluPheGluThrArgPheArgThrPhe 61
400 CGCTGAGGAGGAGCGAGCGAGGATTGAACTGCGTACCGGGCGCATTC 449
62 SerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGln 78
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; Sequence 39, Application US/09277020
; Patent No. 6210892
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
; FILE REFERENCE: ISPH-0339
; CURRENT APPLICATION NUMBER: US/09/277,020
; EARLIER FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 09/167,921
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 926
; TYPE: DNA

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; ORGANISM: Homo sapiens
; US-09-277-020-39

alignment_scores:
  Quality: 428.50      Length: 224
  Ratio: 3.018        Gaps: 4
  Percent Similarity: 63.393      Percent Identity: 40.625

alignment_block:
US-09-155-327E-7 x US-09-277-020-39 ..
Align seq 1/1 to: US-09-277-020-39 from: 1 to: 926

11 ArgAlaLeuValAlaAspPheValGlyTyrlGlyLeuArgGlnGlyTy 27
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400 CGCTGAGGAGGAGCGAGCGAGGATTGAACTGCGTACCGGGCGCATTC 449
62 SerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGln 78
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500 CTTTGAAAGAGTAAAGTAACTCTTCCGGGATGGGGTAAACGTGGGCTC 549
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550 GCATTGTGGCCCTTTTCTCCTCGCGGGGCACTGCTGGAAAGCGTA 599
112 AsnLysGluMetGluProLeuValGlyGlnValGlnGluTrpMetValAl 128
600 GACAAGGAGATGACAGTATGGTGGATCGCATCGAGCTTGATGGCCAC 649
128 aTyrlLeuGluThrArgLeuAlaAspTrpIleHisSerSerGlyTrp 145
650 TTACTCGAATGACCACTGATGGACCTTGATCCAGAGAACGCGGCTGGG 699
145 laGluPheThrAlaLeuTyrlGlyAspGlyAlaLeuGluGlnAlaArg 161
700 ATACTTTTGGAACTATGGGAACAATGACAGCCAGAGCCGGAAG 749
162 LeuArgGlu.....GlyAsnTrpAlaSerValArgThrValLeuThrG 176
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800 CGTGTTCTGCTGGGCTCACTC 821

seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-323-743-1
seq_documentation_block:

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; Sequence 1, Application US/09323743
; Patent No. 6214986
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nikoloff, Brian J.
; APPLICANT: Zhang, Qinglong
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
; FILE REFERENCE: ISPH-0368
; CURRENT APPLICATION NUMBER: US/09/323,743
; EARLIER FILING DATE: 1999-06-01
; EARLIER APPLICATION NUMBER: 09/277,020
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 09/167,921
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)..(836)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: L20121 Genbank
; DATABASE ENTRY DATE: 1994-07-26
; US-09-323-743-1

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alignment_scores:
  Quality: 428.50      Length: 224
  Ratio: 3.018        Gaps: 4
  Percent Similarity: 63.393  Percent Identity: 40.625

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alignment_block:
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Align seg 1/1 to: US-09-323-743-1 from: 1 to: 926

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seq_name: /cqn2.6/ptodata/1/ina/6B.COMB.seq:US-08-461-511A-6

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seq_documentation_block:
; Sequence 6, Application US/08461511A
; Patent No. 6303331

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; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.B.
; TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS
; AND METHODS

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; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESS: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,511A
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: UNKNOWN

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; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARCD:179

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577

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; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..836
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:

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US-08-461-511A-6

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alignment_scores:
  Quality: 428.50      Length: 224

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Thu Jun 6 16:39:21 2002

us-09-155-327e-7.p2n.rn1

Ratio: 3.018 Gaps: 4
Percent Similarity: 63.393 Percent Identity: 40.625

Alignment block:
US-09-155-327e-7 x US-08-461-511A-6

Align seg 1/1 to: US-08-461-511A-6 from: 1 to: 926

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27 r.....
27 CAGCTGAGTCACTTATGATGTGAAAGAACAGAGTGGCCAG 249
200 CAGCTGAGTCACTTATGATGTGAAAGAACAGAGTGGCCAG 33
28 .....ValcysGlyAlaGlyPro 33
28 .....|||.....|||.....|||.....|||.....|||.....
250 AAGGAGTCACTGAGATGAGAGCCCACTGATCAATGCAACCCA 299
34 .....GlyGlnGlyProAlaIasp..... 40
300 TCCTGGACCTGGCAGACAGCCCGGCGTGAATGAGAGCCAG 349
41 .....ProLeuHisGln 45
350 CAGCAGTTGGATGCCCGGAGTGTATCCCATGCGACAGTAAAGCAAG 399
45 lAmelArgAlaIaspGlnPheGlnThrArgPheArgThrPhe 61
45 |||||.....|||.....|||.....|||.....|||.....|||.....
400 CGCTGAGGAGCGAGCGAGTGTGAACCTGCGTACCGCGGCGATC 449
62 SerAspLeuAlaIaspGlnLeuHisValThrProGlySerIleGlnGln 499
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78 gPheThrGlnValSerAspGlnLeuPheGlnGlyProSerIleGlnGln 549
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145 lArgIlePheThrAlaLeuValGlyAlaIaspGlnGlnGlnGlnGln 749
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seq_documentation_block:
Sequence 6, Application PC/TUS9407089.
GENERAL INFORMATION:
APPLICANT: Vertebrate Apoptosis Gene:
TITLE OF INVENTION: Compositions and Methods
TITLE OF INVENTION: Compositions and Methods
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX United States of America
COUNTRY: TX United States of America
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, ASCII
CURRENT APPLICATION DATA: PCT/US94/07089
FILING DATE: CONCURRENTLY FILED
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/081,448
FILING DATE: 22 JUNE 1993
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD090
TELEPHONE: 713-789-2679
TELEFAX: 713-789-2679

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

NAME/KEY: CDS
LOCATION: 135..836
PCT-US94-07089-6

alignment_scores:
Quality: 428.50 Length: 225
Ratio: 3.105 Gaps: 4
Percent Similarity: 61.333 Percent Identity: 41.333

Alignment block:
US-09-155-327e-7 x PCT-US94-07089-6

Align seg 1/1 to: PCT-US94-07089-6 from: 1 to: 926

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11 ArgAlaLeuValAlaIaspheValGlyTyrIysLeuArgGlnIysGlyTyr 27
11 |||||.....|||.....|||.....|||.....|||.....|||.....
150 CGGAGCTGCTGTTGACTTCTCTCTCAAGCTTCCAGAAAGATG 199
27 r.....
27 CAGCTGAGTCACTTATGATGTGAAAGAACAGAGTGGCCAG 249
200 CAGCTGAGTCACTTATGATGTGAAAGAACAGAGTGGCCAG 299
28 .....ValcysGlyAlaGlyPro 35
250 AAGGAGTCACTGAGATGAGAGCCCACTGATCAATGCAACCCA 347
347 CAGCTGAGTCACTTATGATGTGAAAGAACAGAGTGGCCAG 396
44 lAmelArgAlaIaspGlnPheGlnThrArgPheArgThrPhe 60
44 |||||.....|||.....|||.....|||.....|||.....|||.....
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61 PheSerAspLeuAlaIaspGlnLeuHisValThrProGlySerIleGlnGln 77
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94 lYArgLeuValAlaPhePheValPheGlyAlaAlaLeuGlyAlaGly 110
547 GTCCGATTTGGCTTTCTTCCTTCGCGGAGGACGCTGCGGAGAC 596
111 ValAsnLysGluMetGluProLeuValGlyAlaGlnLysMetVal 127
597 GTAGACAAAGAGATGAGATTTGGTGTGATGCGATGCGATGCGATGC 646
127 lAlaTyrLeuGluThrArgLeuAlaAspTyrPheHisSerSerGly 144
647 CACTTACCTGATGACACCTAGACCTTGATCCAGAGAACGCGCGT 696
144 rPalAGluPheThrAlaLeuTyrGlyAspGlyAlaAlaLeuGluAla 160
697 GGGATCTTTGTGAGACTCTATGGACATGCAAGCAGCGGAGAGCGA 746
161 ArgLeuArgGlu.....GlyAsnTyrPalaservalArgThrValLeu 175
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seq_documentation_block:
; Sequence 20, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSER: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1735 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; APPLICATION DATA:
; FILING DATE: 21-FEB-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075

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; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 717 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
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alignment_scores:
Quality: 410.50 Length: 235
Percent Similarity: 59.574 Gaps: 5
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92 sntirpglyargleuvalalaphphevalphneglyalaalaleucysala 108
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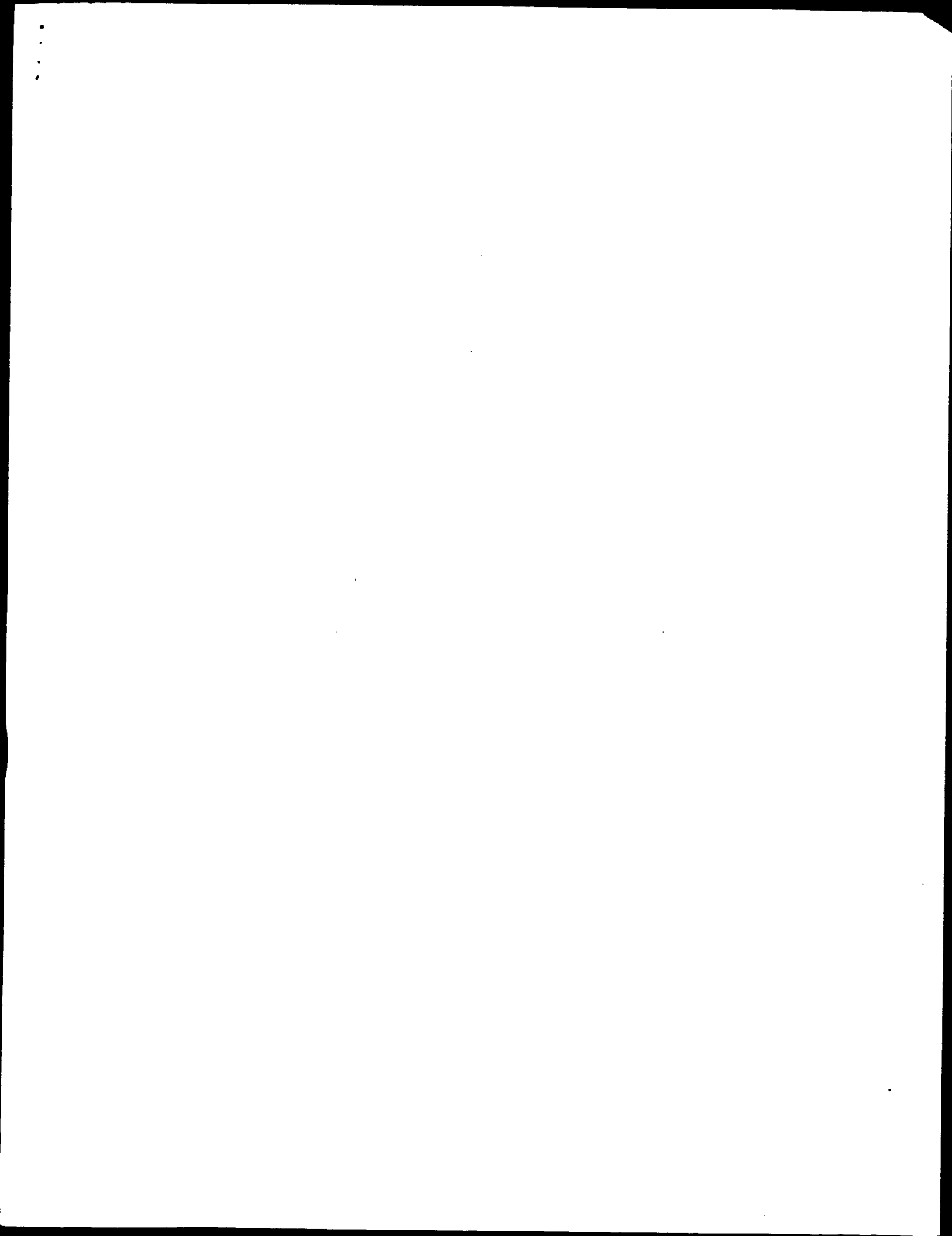
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5' GAGGCGGAGCCCTTGTTGTAAGTGTACGGC.....CCGAGC 2073

Downloaded from <http://ajphaphysocpharm.sagepub.com/> at 11:06 11 November 2014



Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: <http://genome.gsc.riken.go.jp/>, Fax: 81-45-503-9216), Tel: 81-45-503-9222, Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

The cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5', GAGGACGAGAGCATCCCAAGACTCTTTTATTTTATTTCVN 3'], cDNA was prepared by using reverse transcriptase thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGGACGAGATTCGAGGTAAATTAATATTCGCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.

Location/Qualifiers
7 1049

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CDS

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BASE COUNT
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396 a
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Quality:	1000:00	Length:	193
Ratio:	5.181	Gaps:	0

Percent Similarity: 100.000 Percent Identity: 98.964

32/E-7 x AK015644 .

Align seg 1/1 to: AK015644 from: 1 to: 1949

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182 TGTAGGCTTAACTGAGCGCAAGAGGTTACTGTGTGAGACTGGCCCTG 233
34 LysGlnLyrProLaIaLaAspProLeuHISGlnAlaMetArgAlaLaGly 50
232 GGGAAAGCCGACCGCCGACCCGCTGCACCAAGCCATGCGGGCTGTGGA 281
51 AspGlnPheGlnThrArgPheArgArgPheSerAspLeuAlaLaGly 67

282 GACAGAGTTTGAGACCGCTTCCGGCCCGACACTTCTCGACCTGGCCGCTCA 331
67 nLeuHi5ValThrProGlySerAlaIcInIaMrpHeThrgInValSera 84
332 GCTACAGCTACCCCAAGGCTCAAGCCACGACAGACGTTCAACCAAGGTTTCCG 381
84 spGluLeuPheGlnGlyIleProAsnTrpGlyArgLeuValAlaPhePhe 100
382 ACGAACTTTTCCAAAGGGGGCCCTTAACTGGGGCGCTTGTGGACTTCTTT 431
101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnIysGluMetGluTrp 117
432 GTCTTTGGGGCTGCCCTGTGTCTGAGAGCTCAACAAGAAATGAGGCC 481
117 oLeuValIGlyInValGlnGluIuTrpMetValAlaTyrLeuGluIuThrArgT 134
482 TTTGGTGGGCAACAAGTCAGACAGATTGATGTGGCTTACCTCGAACAACGTC 531
134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
532 TGCGTGCAGTGGATCCACAGACAGTGGGGGCGGGCGGAGTTCACAGCTCA 581
151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuAsnArgGlnGlyAsnTrp 167
582 TACGGGGGACGGGGCCCTCGAGAGGACAGCGCGCTCGCGGAGGGGAACTG 631
167 pAlaSerValArgTrpValLeuTrpGlyAlaValAlaLeuGlyAlaLeuVal 184
632 GGCATCACTGAGACAGACTGCTGACGGGGGGCGGTGGCACTGGGGGCCCTTG 681
184 alThrValGlyAlaPhePheAlaSerIys 193
|||||
682 TAACTGTAAGGGGCTTTTGTGTAGCAAG 710

seq_name: gb_htc:AK004680

```
seq_documentation_block:
  locs: 87004500
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	3487 bp	mRNA	linear	HTC 19-JAN-2002
DEFINITION	Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200009L24:Bc12-l like 2, full insert sequence.			
ACCESSION	AK004680			

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (strain)

clone:lib:RIKEN full-length enriched mouse cDNA library
clone:1200009124.

ORGANISM

REFERENCE
1 (sites)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

AUTHORS
 TITLE
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA

Meth. Enzymol. 303, 19-44 (1999)
99279253

MEDLINE 99279253
 PUBMED 10340630

REFERENCE 2 (sites

AUTHORS
Carninci, I

Itch, M., & Norman, J. (1994).

prepare file

JOURNAL
Genome Res

MEDLINE 20499374

PUBMED	11042159
REFERENCE	3 / 614000

Shibata, K.

Комно, Н.,

Sumi, N., I

Yamamoto, R
Fujisaki, A

Yoneda, Y.

Okazaki, Y.

TITLE RIKEN inte

sequencing pipeline with 384 multicapillary sequencer

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1030)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Inceye Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: Image.llnl.gov
Plate: L1CMB00 row: P column: 04
High quality sequence start: 5
High quality sequence stop: 709.
Location/Qualifiers
1. 1030

FEATURES

source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH-MGC-7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAC(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 190 a 284 c 386 g 170 t
ORIGIN

alignment_scores:

Quality: 955.00 Length: 190
Ratio: 5.080 Gaps: 1
Percent Similarity: 98.947 Percent Identity: 97.368

alignment_block:

US-09-155-327e-7 x BE793530 ..

Align seg 1/1 to: BE793530 from: 1 to: 1030

```

1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAlaAsp 17
|||||
144 ATGGGACCCCAAGCTCGGCCCCACACACGGGCTGTGGGCGAGACTT 193
17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProg 34
|||||
194 TGTAGATTATAAGCTGAGGACAGAGGGTTATGTCTGTGGAGACTGGCCCCG 243
34 TylGlyLysProAlaAlaAspProLeuHisGlnAlaMetAlaGlyAlaGly 50
|||||
244 GGGAGGCGCCAGCAGCTACCCAGCTGACCAAGCCAGGCGGCGAGCTGA 293
51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaG 67
294 GATGAGTTCGAGACCCGCTTCGCGCACCTTCCTCATATGCGCGGCTCA 343
67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
|||||
344 GCTGCACTGACCCCGAGGCTAGCCCAACACGCTTCACCCAGGCTCCG 393
84 spGluLeuPheGlnGlyLysProAsnTrpGlyArgLeuValAlaPhePhe 100
394 ATGAACCTTTTCAAGGGGCGCCCAACACTGGGCGGCGCTTGTAGCTTCTT 443

```

```

101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGlnP 117
|||||
444 GTCTTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 493
117 OleuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArg 134
|||||
494 ACTGGTGGGACAAAGTGCAGAGTGTGATGTGCGCTGCTGACAGCGGCG 543
134 eAlaAspTrpLysSerSerGlyTyrPheAlaGluPheThrAlaLeu 150
544 TGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 593
151 TyrGlyAspGlyAlaLeuGluGlnAlaArgArgLeuArgGluGlyAsn 167
594 TACGGGAGCGGCGGCTGAGAGAGCGGCGGCTGCGGAGGAGGAGCTG 643
167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeu 183
644 GGCATCACTGAGACAGTGTGCTGACGGGCGGCTGCTGCTGCTGCTGCT 693
184 ValThrValGlyAlaPhe 189
694 GTAACGTAGGCGGCTTT 711

```

seq_name: gb_est:AL157542

seq_documentation_block:

LOCUS AL157542 804 bp mRNA linear EST 24-FEB-2000
DEFINITION DKFZP761D0816_r1 761 (synonym: hamy2) Homo sapiens CDNA clone
AL157542
VERSION AL157542.1 GI:7057943
KEYWORDS EST.

SOURCE

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 804)
Ansoerge,W., Winkner,U., Mewes,W., Well,B. and Wiemann,S.
EST (Ansoerge,W., Winkner,U., Mewes,W., Well,B. and Wiemann,S.)
Unpublished (1999)
Contact: Ansoerge W
MIPS

Am Kioferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;
Heidelberg/Germany) within the CDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKFZP761D0816) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

source

1. 804
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="DKFZP761D0816"
/clone_lib="761 (synonym: hamy2)"
/tissue_type="amygdala"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT 150 a 217 c 294 g 142 t 1 others
ORIGIN

alignment_scores:

Quality: 953.00 Length: 193
Ratio: 4.964 Gaps: 0
Percent Similarity: 99.482 Percent Identity: 99.482


```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="5218294"
/clone_lip="NH_MGC_118"
/tissue_type="Leukocyte"
/lab_host="DH10B"
/notes="Vector: pcwv-SPORT6; Site_1: NotI; Site_2: EcoRV
(destroyed); RNA source leukocytes from oligo-dT primed
non-activated adult donors. Library is destroyed upon
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(11/1/99)". Research Genetics tracking code 027. Note:

```

seq.documentation_block:	815 bp	mrna	linear	EST 12-JUN-2001
LOCUS	BF785386			
DEFINITION	602111728F1 NCI_CGAP_kid14 Mus musculus cDNA clone IMAGE:4239798			
	5', mRNA sequence.			
ACCESSION	BF785386			
VERSION	BF785386.1	GI:12090422		
KEYWORDS	EST.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 815)			
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .			
TITLE	National Institutes of Health. Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Robert Strausberg, Ph.D.			

Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Inceye Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
 Plate: LLM9853 row: h column: 07
 High quality sequence start: 3
 High quality sequence stop: 650.
 Location/Qualifiers

FEATURES

source

1. 815
 /organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4239798"
 /clone_lib="NCI CGAP Kid14"
 /lab_host="DH10B (r1 phage-resistant)"
 /note="Organ: Kidney; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.75 kb. Constructed by Life
 Technologies. Note: this is a NCI CGAP Library."

BASE COUNT

166 a 212 c 296 g 141 t

ORIGIN

alignment_scores:

Quality: 740.50 Length: 186
 Ratio: 4.114 Gaps: 1
 Percent Similarity: 96.774 Percent Identity: 91.398

alignment_block:

US-09-155-327E-7 x BF785386

Align seg 1/1 to: BF785386 from: 1 to: 815

```

8 ProbspThrArgAlaLeuValAlaAspPheValGlyTyrLeuArgGI 24
3 CCAGACACACGGGCTTAGTGTGACTT. GTAGGCTATAGCTGAGCA 51
24 nLysGlyTyrValCysGlyAlaGlyProGlyGluGlyProAlaAlaasp 41
52 GAAGGTTATGTCCTGTGAGAGTGGCTGGGAGGAGCCCGCCGAC 101
41 TOLUHLSGlnAlaMetArgAlaAlaGlyAspGluPheGluThrArgPhe 57
102 CGCTGCACCAAGCCATGCGGCTGCTGGAGACAGATT. GAGACCCCTTTC 150
58 ArgArgPheSerAspLeuAlaAlaGlnLeuHisValThrProGlyse 74
151 CGCGGCACCTTCTCTGACCTGGCGCTACAGCTACAGTACCCAGGCTC 200
74 TAlaGlnGlnArgPheThrGlnValSerAspGluLeuPheGlnGlyGlyP 91
201 AGCCAGACACAGCTTCACCCAGGTTCCGACGACATTTCCAAAGGGGCC 250
91 TAsnTrpGlyArgLeuValAlaPhePheValPheGlyAlaAlaLeuGly 107
251 CTACTGGGGCCGCTTGTGCGATTCTCTGTGGGGC...TGCTGTGT 297
108 AlaGlnSerValAsnLysGlnMetGluProLeuValGlyGlnValGlnG 124
298 GCTGAGAGTGTCAACAAGAAATGAGCTTG. GTGGGACAGATGTCAAGA 346
124 uTrpMetValAlaTyrLeuGluThrArgLeuAlaAspTrpIleHisSer 141
347 TTGGATGGTGGCTTACCTGAGACAGCTGCTGCTGCTGATTCACACCA 396
141 eTcGlyGlyTyrPalaGluPheThrAlaLeuTyrGlyAspGlyAlaLeuG 157
397 GTGGGGGCTGGCGGAGTTTACAGCTTATACGGGGAGCGGGCCCTGTAG 446

```

158 GluAlaArgArgLeuArgGluGlyAsnTrpAlaSerValArgThrValle 174
 447 GAGGACAGGCT. CTGGGGAGGGGAGGAGCG. GCATGATGAGACAGTCT 494
 174 uThrGlyAlaValAlaLeuGlyAlaLeuValThrValGlyAlaPhePhe 191
 495 GAGGGGGCGCTGGGACT. GGGGCGCTGTACTGTAGGGCGCTTTTGC 543
 191 laSerLys 193
 544 TAGCAGCT 551
 seq_name: gb_est2:BG298789

seq_documentation_block:

LOCUS BG298789 792 bp mRNA linear EST 21-FEB-2001
 DEFINITION 602396527F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4511215 5',
 mRNA sequence.
 ACCESSION BG298789
 VERSION BG298789.1 GI:13063794
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE

1 (bases 1 to 792)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 Mammalia: Eutharia: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 EMAIL: cgabs-r@mail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Inceye Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
 Plate: LLM10394 row: e column: 08
 High quality sequence stop: 713.

FEATURES

source

1. 792
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:4511215"
 /clone_lib="NIH_MGC_94"
 /tissue_type="retina"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally; Oligo-dT primed.
 Average insert size 3.3 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."
 BASE COUNT 174 a 201 c 246 g 171 t
 ORIGIN

alignment_scores:

Quality: 733.00 Length: 146
 Ratio: 5.055 Gaps: 0
 Percent Similarity: 99.315 Percent Identity: 97.945

alignment_block:

US-09-155-327E-7 x BG298789

Align seg 1/1 to: BG298789 from: 1 to: 792

```

1 MetAlaThrProAlaSerAlaProspThrArgAlaLeuValAlaAsp 17
99 ATGGGAGACCCGCTCAACCCAGACACAGGCGCTCTAGTGGCTGACTT 148
17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyPro 34

```


ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 758)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Inqyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: L1AM11477 row: a column: 01
High quality sequence stop: 753.

FEATURES

Source

Location/Qualifiers
1..758
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5190792"
/clone_1bp="NIH-MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:
PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH-MGC Library."

BASE COUNT

140 a 216 c 228 g 174 t

alignment_scores:

Quality: 583.00 Length: 112
Ratio: 5.205 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.107

alignment_block:

US-09-155-327E-7 x B1764428 ..

Align seg 1/1 to: B1764428 from: 1 to: 758

```

1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
|||||
139 ATGGCGACCCCGCTCGGCCACACACGGGCTGCTGGCAGACTT 188
|||||
17 eValGlyTyrLeuAlaArgLysGlyTyrValCysGlyArgProG 34
|||||
189 TGTAGGTTATAGCTGAGCAGAGAAGGTTATCTGTGTGAGCTGCCCG 238
|||||
34 LysLysLysProAlaAlaAspProLeuHisGlnAlaMetArgAlaLagly 50
|||||
239 GGGAGGGCCCGACGCTGACCCGCTGCACCAAGCATGGGGCAGCTGGA 288
|||||
51 AspGluPheGluThrArgPheArgThrPheSerAspLeuAlaLagly 67
|||||
289 GATGACTTGGAGACCCGCTTCCGGCCACCTTCTGTGATCTGGCGCTCA 338
|||||
67 IleuHisValThrProGlySerAlaGlnArgPheThrGlnValSera 84
|||||
339 GCTGATGTGACCCCGCTCAGCCCAACAGCTTCACCCAGGCTCCG 388
|||||
84 spGluLeuPheGlnGlyProLeuThrProGlyArgLeuValAlaPhePhe 100
|||||
389 ATGACATTTTCAAGGGGGCCCAACTGGGGCCGCTTGTAGCCTTCTTT 438

```

101 ValPheGlyValAlaLeuCysAlaGluSerValAsn 112
|||||
439 GTCTTTGGGCTCGACTGTGTGCTGAAGTGTTCC 474

seq_name: gb-est2:BM191403

seq_documentation_block:

LOCUS BM191403 601 bp mRNA linear EST 11-DEC-2001
DEFINITION d3186a10.y1 NICHD XGC L11 Xenopus laevis cDNA clone IMAGE:5129754
5' similar to SW:ARL_XENLA 091827 APOPTOSIS REGULATOR R1 ;, mRNA
Sequence.

ACCESSION BM191403
VERSION BM191403.1 GI:17527366
KEYWORDS EST.

SOURCE African clawed frog.
Xenopus laevis

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 601)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Seq primer: 40RP from Gibco

High quality sequence stop: 386.
Location/Qualifiers
1..601

FEATURES

Source

/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:5129754"
/clone_1bp="NICHD XGC L11"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: PCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection (XGC
) library."

BASE COUNT 149 a 125 c 189 g 138 t

alignment_scores:

Quality: 571.50 Length: 164
Ratio: 4.112 Gaps: 1
Percent Similarity: 84.756 Percent Identity: 66.463

alignment_block:

US-09-155-327E-7 x BM191403 ..

Align seg 1/1 to: BM191403 from: 1 to: 601

```

11 ArgAlaLeuValAlaAspPheValGlyTyrLysLeuAlaGlnLysGlyTyr 27
|||||
119 CGGGCTTTGGTGAGAGATTTTGTGGTACAGATTATGCCAACCTACTCT 168
|||||
27 rValCysGlyLaglyProGlyGluGlyProAlaAlaAspProLeuHisG 44
|||||
169 TGT.....CCAGAGCTGCAGAGACGACGATCTCTGCTTGCATT 209
|||||
44 InAlaMetArgAlaLaglyAspGluPheGluThrArgPheArgArgThr 60
|||||
210 CAGCTATGCTGCTGCAGGGAGTGAATTGAGAGCGATTCAAGACAAGCA 259

```


DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: L1CM987 row: d column: 05
 High quality sequence stop: 561.

FEATURES
 source Location/Qualifiers

1..601
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4106836"
 /clone_lib="NIH MGC 17"
 /tissue_type="rhodomyosarcoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: muscle; Vector: pOT7; Site_1: EcoRI;
 Site_2: XhoI; CDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G) size-selected >500bp
 for average insert size 1.8kb. Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 BASE COUNT 110 a 176 c 201 g 114 t
 ORIGIN

alignment_scores:
 Quality: 568.50 Length: 147
 Ratio: 4.274 Gaps: 7
 Percent Similarity: 90.476 Percent Identity: 85.714

alignment_block:
 US-09-155-327E-7 x BF204905

Align seg 1/1 to: BF204905 from: 1 to: 601

4 ProbaSerAlaProasp...ThrArgAlaLeuValAlaasp.PheValG 19
 |||||
 165 CCAGCCCTGCGCCCGCCAGCACCGGCTGCTGGCAGACATTTGTG 214
 19 lYTrIysLeuArgGlnIysGlyTyrValGlyGlyAlaGlyProGlyGlu 35
 |||||
 215 GTTATAGCTGAGCGACAGAGGTTATGCTGTGAGAGCTGCGCGGAG 264
 36 GlyProAlaAlaaspProLeuHisGlnAlaMetArgAlaAlaGlyASP1 52
 |||||
 265 GGCCTCAGCAGCTGACCCACTGACCAAGCCATGCGGAGCAGTGGAGATGA 314
 52 upheGluThrArgPheArgArg...ThrpheSerAspLeuAlaGlnLeu 68
 |||||
 315 GTTCGAGACCCCGCTTCGCGCTCCTCTGATCTGCGGCTCAGCTG 364
 69 HisValThrProGlySerAlaGlnArg.PheThrGlnValSerasp 84
 |||||
 365 TCATGTGATCCAGGCTCAGCCCAACAGACTTACCAGAGTCTCCGAT 414
 85 GluLeuPhe.GlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePheV 101
 |||||
 415 GAACTGTTTGCAGAGGGGCCCACTGGGCTTCCCTTACCTCTTGG 464
 101 aPheGlyAlaAlaLeuGlyAlaGlySerValAsnIysGlnMetGluPro 117
 |||||
 465 TCTTGGGGGCTGCACCTGTGCTGAGAGCTGCAACAAGAGATGGAACA 514
 118 LeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgLe 134
 |||||
 515 CTGGTGGGACAGAGTGCAGAGTGTGCTGCTGAGAGCGGCTCT 564
 134 uAlaasp.TripLeHisSerSerGlyGly 143
 |||||
 565 GCGTATCTGATCCAAAGAGAGTGGGT 593
 seq_name: gb_est2:BE508939

seq_documentation_block:

LOCUS BE508939 612 bp mRNA linear EST 07-AUG-2000

DEFINITION dc1409.y1 NICHD XGC L11 Xenopus laevis CDNA clone IMAGE:3397121 5' sequence similar to SW:ARL_XENLA 091827 APOPTOSIS REGULATOR R1 ;, mRNA

ACCESSION BE508939

VERSION BE508939.1 GI:9728714

KEYWORDS EST.

SOURCE African clawed frog.

ORGANISM Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

Xenopodinae; Xenopus.

1 (bases 1 to 612)

NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgap@r-email.nih.gov

Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: Xenopus clones from this library are available

through the I.M.A.G.E. Consortium/LLNL at: infoimage.llnl.gov

Seq primer: -40RP from Glibco

High quality sequence stop: 439.

Location/Qualifiers

1..612

/organism="Xenopus laevis"

/db_xref="taxon:8355"

/clone="IMAGE:3397121"

/clone_lib="NICHD XGC L11"

/lab_host="DH10B (phage-resistant)"

/note="Organ: liver; Vector: PCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: oligo dT.
 Average insert size 1.4 kb. Constructed by Life
 Technologies. Note: This is a Xenopus Gene Collection (XGC
) library."

BASE COUNT 154 a 128 c 188 g 141 t 1 others

ORIGIN

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Percent Similarity: 81.928 Percent Identity: 62.651

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 27 rValGlyGlyAlaGlyProGlyGlnGlyProAlaAlaaspProLeuHisG 44
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 61 PheSerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGln 77
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 262 TTCAGTGAATCTCCACACAGATCCAGTGAATCCCGGACACAGATATGC 311
 77 nArgPheThrGlnValSerAspGluLeuPheGlnGlyGlyProAsnTrpG 94
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 312 ACGATTGCTGAGTACAGTAGTACCTGTTCCAGAGAGGGTGAATTTCG 361

us-09-155-327e-7.p2n.rst

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127  1AaArgLeuGluThrArgLeuAlaAspTyrPheHisSerSerGlyGlyT 144
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462  GACATTTCTGGAGACAAACCTGAGAGCGCTGGATTCAGAACATGGAGGCT 511
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144  rPalGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArg 160
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512  TGAATGATTTCTAACTCTAATATGAGGATGGTGCATAGAAAGCCAGG 561
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161  ArgLeuArgGlnGlyAsnTyrAlaSerValAlaArgThrValLeuThrGly 176
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AC AAV28334;
XX
DT 02-OCT-1998 (first entry)
XX
DE Human bcl-2 gene.
XX
KW ss; bcl-2; cell death pathway; apoptotic; apoptosis; human.
XX
OS Homo sapiens.
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FT /product= bcl-2
FT /note= "No stop codon given"
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PN US5789201-A.
XX
PD 04-AUG-1998.
XX
PF 11-FEB-1997; 97US-0798897.

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XX 23-FEB-1996; 96US-0012201.
PR 11-FEB-1997; 97US-0798897.
XX
XX (COCE-) COCENSYS INC.
XX
XX Guastella J;
XX WPI: 1998-446079/38.
XX P-PSDB: AAM61392.
XX
XX Nucleic acids encoding B-cell lymphoma-2 protein - useful for
XX producing recombinant protein for use in treating uncontrolled cell
XX growth e.g. cancers
XX
XX Claim 3; Column 15/16; 27pp; English.
XX
XX The mammalian bcl-2 genes encode a protein that is a member of the bcl-2
XX family, components in the cell death pathway. The bcl-2 family
XX have both apoptotic activity and the apoptosis blocking activity. bcl-2
XX falls in the apoptosis activity category. The recombinant protein may
XX be used to prevent uncontrolled cell growth, either by its direct
XX administration to recombinant genetic constructs to increase its
XX expression in vivo. Also, antisense constructs can be used in disorders
XX where prevention of cell death is desired.
XX
XX Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;

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alignment_scores:
  Quality: 1002.00      Length: 193
  Ratio: 5.219          Gaps: 0
  Percent Similarity: 99.482  Percent Identity: 99.482

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alignment_block:

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51 TGTAGGTTATTAAGCTGAGGAGAAAGGGGTATGTCTGTGAGCTGGCCCG 100
34 1ygluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
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|||||
151 GATGAGTTCAGACCCGCTTCGCGCCACCTCTCTGATCTGGCCGCTCA 200
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201 GCTGATGTGACCCAGGCTCAGCCCAACACAGCTTCACCCAGGTCGCG 250
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301 GCTTTGGGGGCTGCACTGTGTCTGAGAGTGTCAACAAAGAGATGGAACC 350
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 ID AAK15946 standard; cDNA: 579 BP.
 AC AAK15946;
 XX 20-MAY-1999 (first entry)
 DE cDNA encoding the human bcl-2 protein.
 XX Rat bcl-2 protein; Rbcl-2: human bcl-2 protein; Hbcl-2: bcl-2 homologue;
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
 KW head trauma; Alzheimer's Disease; muscular degenerative disease;
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
 KW premature cell death; cell death stimulator; prolonged cell life span;
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
 KW parasite; ss.
 XX Homo sapiens.
 OS US5883229-A.
 PN 16-MAR-1999.
 PD 25-NOV-1997; 97US-0978523.
 PF 23-FEB-1996; 96US-0012201.
 PR 11-FEB-1997; 97US-0798897.
 PR 25-NOV-1997; 97US-0978523.
 XX (COCE-) COCENSYS INC.
 PA Guastella J;
 PI WPI: 1999-214150/18.
 DR P-PSDB: AAW97392.
 DR Novel bcl-2 homologues of the rat and human bcl-2 protein - useful
 PT for modulating programmed cell death
 PS Disclosure: Columns 15-16; 26pp; English.
 XX The present sequence encodes human bcl-2 protein (Hbcl-2). The
 CC specification also describes rat bcl-2 protein (Rbcl-2). Rbcl-2 and
 CC Hbcl-2 are homologues of the bcl-2 protein thought to be involved in
 CC programmed cell death (apoptosis and necrosis). Rbcl-2 and Hbcl-2
 CC proteins may be used to treat conditions associated with a disruption of
 CC the cell death pathway. If they act as cell death inhibitors, they may be
 CC used in therapies to treat subjects suffering from: strokes, head trauma,
 CC Alzheimer's Disease, neural and muscular degenerative diseases
 CC (especially multiple sclerosis), myocardial infarction, vitally induced
 CC cell death, aging, spinal cord injuries and amyotrophic lateral
 CC sclerosis-conditions where cells under go premature cell death as a
 CC result of triggers which may or may not be apparent. They may also be
 CC used in this way to develop cell lines which remain viable in culture for
 CC an extended period. In contrast, if they act as cell death stimulators,
 CC Rbcl-2 and Hbcl-2 may be used to treat conditions associated with

CC prolonged cell life span such as cancer (especially Kaposi's sarcoma and
 CC lung cancer) and auto/hyperimmune diseases. They may also be used to
 CC cause cell death in, and hence control, parasites.
 XX Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;
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 Quality: 1002.00 Length: 193
 Ratio: 5.219 Gaps: 0
 Percent Similarity: 99.482 Percent Identity: 99.482
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 451 TACGGGAGCGGGCCCTGAGAGAGCGGCGCTGCGGAGGAGGAGCTG 500
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 ID AAK25133 standard; DNA: 581 BP.
 AC AAK25133;
 XX 05-JUL-1999 (first entry)
 DT

XX Mouse bcl-w gene.
 DE
 XX
 KW Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
 animal model; ss.
 XX
 OS Mus sp.
 PN W09913710-A1.
 XX
 PD 25-MAR-1999.
 XX
 PF 16-SEP-1998; 98MO-AU00764.
 XX
 PR 16-SEP-1997; 97AU-0009228.
 XX
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PI Adams J, Cory S, Gibson L, Koentgen F, Print C;
 DR WPI: 1999-243890/20.
 DR P-PSDB: AAY05531.
 XX
 PS Claim 3; Page 34; 52pp; English.
 CC The present sequence is the mouse bcl-w gene encoding Bcl-w protein
 CC (see AA005531), a pro-survival member of the Bcl-2 family which is
 CC widely expressed and which is essential for spermatogenesis. The
 CC invention relates generally to a method of treatment and to an
 CC animal model for the identification of molecules and genetic
 CC sequences useful for inducing or reducing fertility of male
 CC animals. Methods are provided for the treatment of infertility, or
 CC for reducing fertility, by modulating spermatogenesis. An animal
 CC model carries a mutation is at least one allele of the human or
 CC murine bcl-w gene or in a gene associated with bcl-w. Such animals
 CC have disorganized seminiferous tubules and are substantially
 CC infertile, but possess no other major abnormalities as determined
 CC by histological examination. They can be used to screen for
 CC therapeutic molecules including genetic sequences capable of
 CC inducing, enhancing or otherwise facilitating spermatogenesis in
 CC animals, or which can induce infertility.
 CC
 SO Sequence 581 BP; 106 A; 158 C; 200 G; 117 T; 0 other;

alignment_scores:
 Quality: 1000.00 Length: 193
 Ratio: 5.181 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 98.964

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Align seg 1/1 to: AAX25133 from: 1 to: 581

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67 nLeuHisValThrProGlySerAlaGlnGlnAlaArgPheThrGlnValSerA 84
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251 ACGACTTTTCCAGAGGGGCCCTTAAGTGGGCGCTGTGTGGCATTTCTT 300
101 ValPheGlyAlaAlaLeuCysAlaGluSerValaLeuLysGluMetGluPr 117
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117 oLeuValGlyGlnValGlnGluThrPheValAlaTyrLeuGluThrArgL 134
351 TTTGGTGAGACAAAGTCCAGAGTGGATGTGGCTTACCTGGAGACAGTC 400
134 eValAspTrpIleHisSerSerGlyTyrPAlaGluPheThrAlaLeu 150
401 TGGCTGACTGGATCCACAGCAGTGGGGCTGGGCGAGTTCCACAGCTCTA 450
151 TyrGlyAspGlyAlaLeuGluGluAlaAlaArgArgLeuArgLysAsnTr 167
451 TACGGGAGACGGGGCCCTGAGAGGAGCAGCGCTGCGGAGGGAACCTG 500
167 PAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeu 184
501 GGCACTCACTGAGACAGTGCAGACGGGGCGCGTGGCACTGGGGCCCTGG 550
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 AC AA196577;
 XX
 DT 22-APR-1998 (first entry)
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 DE Human bcl-w DNA.
 XX
 KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
 KW diagnosis; degenerative disease; ss.
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 PN W09735971-A1.
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 PD 02-OCT-1997.
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 PF 27-MAR-1997; 97MO-AU00199.
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 PR 27-MAR-1996; 96AU-0008965.
 XX
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PI Adams JM, Cory S, Gibson LM, Holmgren SP;
 DR WPI: 1997-489635/45.
 DR P-PSDB: AAM36047.
 XX
 PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce
 PT or inhibit cell survival, e.g. for treatment of cancer and
 XX degenerative diseases

PS Claim 3: Page 48; 86pp; English.

XX This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene
CC family, extracted from an adult brain library. This gene promotes cell
CC survival, so its modulation is useful in treatment of cancer or
CC auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's
CC disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia,
CC human immunodeficiency virus infection or in cell transplants.
CC up-regulation of the gene can also be used to modify cell lines cultured
CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas
CC and to increase survival of primary explants during genetic modification.
CC It can be used to produce recombinant Bcl-w for therapy, diagnosis,
CC antibody production or screening of potential modulators.

XX Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other:

alignment_scores: Length: 193
Quality: 1000.00 Gaps: 0
Ratio: 5.181

Percent Similarity: 100.000 Percent Identity: 98.964

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Align seg 1/1 to: AAT96577 from: 1 to: 583

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117 cLeuValGlyGlnValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG 134
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151 TyrGlyArgGlyAlaLeuGlnGlnAlaArgArgLeuArgGlnGlyAsnTr 167
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551 TAACCTAGGGGCTTTTGTCTACAGAG 579

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seq_documentation_block:

ID AAX25134 standard; DNA; 583 BP.

AC AAX25134;

DT 05-JUL-1999 (first entry)

DE Human bcl-w gene derivative.

XX Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;

KW animal model; ss.

OS Homo sapiens.

PN WO913710-A1.

PD 25-MAR-1999.

PF 16-SEP-1998; 98WC-AU00764.

PR 16-SEP-1997; 97AU-0009228.

PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

XX Adams J, Cory S, Gidson L, Koentgen F, Print C;

XX WPL: 1999-243890/20.

DR P-PSDB; AAY05532.

PT An animal model exhibiting reduced levels of a Bcl-w protein and/or

XX protein associated with Bcl-w

XX Disclosure; Page 36; 52pp; English.

XX The present sequence is described as a derivative of the human
XX bcl-w gene (see AAX25132) and encodes Bcl-w protein (see AAY05532), a
XX pro-survival member of the Bcl-2 family which is widely expressed
XX and which is essential for spermatogenesis. The invention relates
XX generally to a method of treatment and to an animal model for the
XX identification of molecules and genetic sequences useful for
XX inducing or reducing fertility of male animals. Methods are
XX provided for the treatment of infertility, or for reducing
XX fertility, by modulating spermatogenesis. An animal model carries
XX a mutation is at least one allele of the human or murine bcl-w gene
XX or in a gene associated with bcl-w. Such animals have disorganised
XX seminiferous tubules and are substantially infertile, but possess no
XX other major abnormalities as determined by histological examination.
XX They can be used to screen for therapeutic molecules including
XX genetic sequences capable of inducing, enhancing or otherwise
XX facilitating spermatogenesis in animals, or which can induce
XX infertility.

XX Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other:

alignment_scores: Length: 193
Quality: 1000.00 Gaps: 0
Ratio: 5.181

Percent Similarity: 100.000 Percent Identity: 98.964

alignment_block:
US-09-155-327e-7 x AAX25134 ..

Align seg 1/1 to: AAX25134 from: 1 to: 583

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67 nLeuHisValThrProGlySerAlaGlnAlaRphPheThrGlnValSera 84
  |||
201 GCTGCAATGTGACCCCGCTCAGCCAGCAAGCCTTCAACCCAGCTCTCCG 250
  |||
84 sPGLuLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
  |||
251 ACGAACTTTTTCAGAGGGGCCCAACTGGGGCCCTTGTAGCCCTCTTT 300
  |||
101 ValPheGlyAlaAlaLeuCYsAlaGlnSerValAsnLYsGluMetGluPr 117
  |||
301 CTCCTTGGGGCTGCACTGTGTCTGAGAGTGTCAACAAGAGATGGAACC 350
  |||
117 oLeuValGIYGIYValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
  |||
351 ACTGGTGGACAGTGCAGAGTGTGATGTGCTTACCTGGAGACGGCGC 400
  |||
134 eUAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
  |||
401 TGGTGCAGTGTGATCCACAGCAGTGGGGGCTGGGGAGTTCCACAGCTTA 450
  |||
151 TyrGIYAspGIYAlaLeuGluGlnAlaArgArgLeuArgGluGlyAsnTr 167
  |||
451 TACGGGGAGGGGGCCCTGGAGAGCGCGGCTCTGGGAGGGGAACCTG 500
  |||
167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuY 184
  |||
501 GGCATCAGTGTAGACAGTGTGACGAGGGGGCCCTGGAGCTGGGGCCCTGG 550
  |||
184 aLTPheGlyAlaAlaPhePheAlaSerLYs 193
  |||
551 TAACTGTAGGGGCTTTTGTGTAGCAAG 579
  |||
seq_name: /SIDSI/gcgdata/geneseq/geneseqn.embl/NA1998.DAT.AAV28333
seq_documentation block:
ID AAV28333 standard: cDNA, 579 BP.
AC AAV28333;
XX
DT 02-OCT-1998 (first entry)
DE Rat bcl-2 gene.
XX
KM ss: bcl-2; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
XX
OS Rattus sp.
XX
FH Key 1..579 Location/Qualifiers
FT CDS /tag= a
FT /product= bcl-2
FT /note= "No stop codon given"
XX
PN US5789201-A.
XX
PD 04-AUG-1998.
XX
PF 11-FEB-1997; 97US-0798897.
XX
PR 23-FEB-1996; 96US-0012201.
PR 11-FEB-1997; 97US-0798897.
PR

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```

XX
PA (CODE) COGENS INC.
XX
PI Guastella J;
XX
DR WPI: 1998-446079/38.
XX
DR P-PSDB: AAM61391.
XX
PT Nucleic acids encoding B-cell lymphoma-y protein - useful for
PT producing recombinant protein for use in treating uncontrolled cell
PT growth e.g. cancers
XX
XX
PS Claim 2: Column 13/14; 27pp; English.
XX
XX
CC The mammalian bcl-2 genes encode a protein that is a member of the bcl-2
CC family, components in the cell death pathway. The bcl-2 family
CC have both apoptotic activity and the apoptosis blocking activity. bcl-2
CC falls in the apoptosis activity category. The recombinant protein may
CC be used to prevent uncontrolled cell growth, either by its direct
CC administration to recombinant genetic constructs to increase its
CC expression in vivo. Also, antisense constructs can be used in disorders
CC where prevention of cell death is desired.
XX
XX
SO Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 other;

alignment_scores:
Quality: 996.00 Length: 193
Ratio: 5.161 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 98.446

alignment block:
US-09-155-327E-7 x AAV28333 ..
Align seg 1/1 to: AAV28333 from: 1 to: 579

1 MetaLathrProAlaSerAlaProAspThrArgAlaLeuValAlaAspH 17
  |||
1 ATGGCGACCCCGAGCTTCAACCCAGACACAGGGGCTGTAGTGGCTGACT 50
  |||
17 eValGIYrLYsLeuArGInLYsGIYrValLYsGIYAlaGIYProG 34
  |||
51 TGTAGGTTATAGCTGAGCAGAAAGGTTATGTCTGTGAGCTGGCCCTG 100
  |||
34 LYGIUGLYProAlaAlaAspProLeuHisGlnAlaMetArGAlaAGly 50
  |||
101 GGGAGGGCCAGCAGCTGACCCCTCCACCAAGCCATGGGGAGCTGTA 150
  |||
51 AspGluPheGluThrArGArGThrPheSerAspLeuAlaAlaGI 67
  |||
151 GACGAGTTTGAGACCCCGCTTCGGGGCAGCTTCTGTGACTGGCCGCTCA 200
  |||
67 nLeuHisValThrProGlySerAlaGlnAlaRphPheThrGlnValSera 84
  |||
201 GCTACACGTGACCCCGAGCTCAGCCAGCAAGCCTTCAACCCAGCTTCCG 250
  |||
84 sPGLuLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
  |||
251 ACGAACTTTTTCAGAGGGGCCCAACTGGGGCCCTTGTAGCCCTCTTT 300
  |||
101 ValPheGlyAlaAlaLeuCYsAlaGlnSerValAsnLYsGluMetGluPr 117
  |||
301 CTCCTTGGGGCTGCACTGTGTCTGAGAGTGTCAACAAGAGATGGAACC 350
  |||
117 oLeuValGIYGIYValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
  |||
351 ATTGGTGGACAGTGCAGAGTGTGATGTGCTTACCTGGAGACAGCTCT 400
  |||
134 eUAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
  |||
401 TGGCTGAGTGTGATCCACAGCAGTGGGGGCTGGGGAGTTCCACAGCTTA 450
  |||
151 TyrGIYAspGIYAlaLeuGluGlnAlaArgArgLeuArgGluGlyAsnTr 167
  |||

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|||||
451 TACGGGAGCGGGCCCTGGAGAGGACGGCGCTGCGGGAGGGAATG 500
167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
|||||
501 GGCACTACGTAGAGACAGTCTGACGGGGCTGTGGCACTGGGGCCCTGG 550
184 aThrValGlyAlaPhePheAlaSerLys 193
|||||
551 TAACTGTAGGGGCTTTTGTGCTAGCAAG 579
seq_name: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AA15945

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seq_documentation_block:
ID   AAX15945 standard; cDNA, 579 BP.
XX
XX   AAX15945;
AC
XX   20-MAY-1999 (first entry)
DE
XX   cDNA encoding the rat bcl-2 protein.
XX
XX   Rat bcl-2 protein; Rbcl-2; human bcl-2 protein; Hbcl-2; bcl-2 homologue;
KM   programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KM   head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KM   multiple sclerosis; myocardial infarction; vitally induced cell death;
KM   aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KM   premature cell death; cell death stimulator; prolonged cell life span;
KM   Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
KM   parasite; ss.
XX
XX   Rattus sp.
OS
XX   US5883229-A.
XX   16-MAR-1999.
PD
XX
XX   25-NOV-1997; 9705-0978523.
PF
XX
XX   23-FEB-1996; 9605-0012201.
PR
XX   11-FEB-1997; 9705-0798897.
PR
XX   25-NOV-1997; 9705-0978523.
PR
XX   (COCE-) COCENSYS INC.
PA
XX   Guastella J;
PI
XX   WPI: 1999-214150/18.
DR
XX   P-PSDB; AAM97391.
PT
XX   Novel bcl-2 homologues of the rat and human bcl-2 protein - useful
XX   for modulating programmed cell death
XX
XX   Disclosure: Columns 13-16; 26pp; English.
PS
XX
XX   The present sequence encodes rat bcl-2 protein (Rbcl-2). The
XX   specification also describes human bcl-2 protein (Hbcl-2). Rbcl-2 and
XX   Hbcl-2 are homologues of the bcl-2 protein thought to be involved in
XX   programmed cell death (apoptosis and necrosis). Rbcl-2 and Hbcl-2
XX   proteins may be used to treat conditions associated with a disruption of
XX   the cell death pathway. If they act as cell death inhibitors, they may be
XX   used in therapies to treat subjects suffering from: strokes, head trauma,
XX   Alzheimer's Disease, neural and muscular degenerative diseases
XX   (especially multiple sclerosis), myocardial infarction, vitally induced
XX   cell death, aging, spinal cord injuries and amyotrophic lateral
XX   sclerosis conditions where cells under go premature cell death as a
XX   result of triggers which may or may not be apparent. They may also be
XX   used in this way to develop cell lines which remain viable in culture for
XX   an extended period. In contrast, if they act as cell death stimulators,
XX   Rbcl-2 and Hbcl-2 may be used to treat conditions associated with
XX   prolonged cell life span such as cancer (especially Kaposi's sarcoma and
XX   lung cancer) and auto/hyperimmune diseases. They may also be used to
XX   cause cell death in, and hence control, parasites.

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```

XX
SQ   Sequence 579 BP: 111 A; 157 C; 198 G; 113 T; 0 other;
      alignment_scores:
          Quality: 996.00      Length: 193
          Ratio: 5.161        Gaps: 0
      Percent Similarity: 100.000      Percent Identity: 98.446
      alignment_block:
      US-09-155-327e-7 x AAX15945 ..
      Align seg 1/1 to: AAX15945 from: 1 to: 579

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1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspH 17
|||||
1 ATGGCGACCCACGCTCAACCCAGACACAGCGGCTCTAGTGGCTGACTT 50
17 eValGlyTyrLysLeuArgGlnLysGlyTyrValLysGlyAlaGlyProG 34
|||||
51 TGTAGGCTATAGCTGAGACAGAGGTTATGTTGTGGAGCTGGCCCTG 100
34 LyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
|||||
101 GGGAAGGCCAGCAGCCGACCGCTGCACCAACCATGGCGGAGCTGGA 150
101 GGGAAAGGCCAGCAGCCGACCGCTGCACCAACCATGGCGGAGCTGGA 150
51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaIaG 67
151 GACGAGTTTGAGACCCGCTTCGGCGCACCTTCTGACCTGGCCGCTCA 200
67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
|||||
201 GCTACAGCTGACCCAGGCTCAGCCAGCAACGCTTACCAGGTTCCG 250
84 SPGLuLeuPheGlnGlnLysLysProAsnTrpGlyArgLeuValAlaPheP 100
251 ACGAACTTTTCCAGGGGGCCCAACTGGGCGCGCTTGTGGCAFTCTTT 300
101 ValPheGlyAlaAlaLeuLysAlaGlnSerValAsnLysGluMetGluP 117
|||||
301 GTCTTTGGGCTGCCCTGTGTCTCAGAGTGCACAAAGAAATGAGACC 350
117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
351 ATTGGTGGGACAAAGTCAGATGATGTGATCTACCTGGAGACAGCT 400
134 euAlaAspTrpPheHisSerSerGlyLysTrpAlaGluPheThrAlaLeu 150
401 TGGCTGACTGATCCACAGCAGTGGGGCTGGCGGAGTTCACAGCTCTA 450
151 TyrGlyAspGlyAlaLeuGlnGluAlaArgArgLeuArgGluGlyAsnTr 167
451 TACGGGAGCGGGCCCTGGAGAGGACGCGCTGCGGAGGGAACCTG 500
167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
|||||
501 GGCACTACGTAGAGACAGTCTGACGGGGCTGTGGCACTGGGGCCCTGG 550
184 aThrValGlyAlaPhePheAlaSerLys 193
551 TAACTGTAGGGGCTTTTGTGCTAGCAAG 579
seq_name: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:AA196578
seq_documentation_block:
ID   AAT96578 standard; DNA; 581 BP.
XX
XX   AAT96578;
AC
XX   22-APR-1998 (first entry)
DE
XX   Mouse bcl-2 DNA.
XX

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KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
 XX diagnosis; degenerative disease; ss.
 OS Mus sp.

Key Location/Qualifiers
 CDS 1..507
 FT /*tag= a
 FT /product= bcl-w
 FT /note= "q"

W09735971-A1.

02-OCT-1997.

27-MAR-1997; 97WO-A000199.

27-MAR-1996; 96AU-0008965.

(AMRA-) AMRAD OPERATIONS PTY LTD.

PI Adams JM, Cory S, Gibson LM, Holmgren SP;

DR WPI; 1997-489635/45.

DR P-PSDB; AAW36048.

PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce
 PT or inhibit cell survival, e.g. for treatment of cancer and
 PT degenerative diseases

XX Claim 3; Page 50-51; 86pp; English.

CC This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene
 CC family. This gene promotes cell survival, so its modulation is useful in
 CC treatment of cancer or auto-immune diseases, degenerative diseases (e.g.
 CC stroke, Alzheimer's disease, myocardial infarct, muscular degeneration,
 CC hypoxia, ischaemia, human immunodeficiency virus infection or in cell
 CC transplants. Up-regulation of the gene can also be used to modify cell
 CC lines cultured in vivo, e.g. to develop new lines; to facilitate
 CC isolation of hybridomas and to increase survival of primary explants
 CC during genetic modification. It can be used to produce recombinant Bcl-w
 CC for therapy, diagnosis, antibody production or screening of potential
 CC modulators.

SO Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 other;

alignment_scores:

Quality: 965.00 Length: 193
 Ratio: 5.079 Gaps: 0
 Percent Similarity: 98.446 Percent Identity: 94.819

alignment_block:

US-09-155-327e-7 x AAT96578

Align seg 1/1 to: AAT96578 from: 1 to: 581

1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
 ||| |||||||||:|||||
 1 ATGCCGACCCCAAGCTCAACCCAGACACACGCGCTAGTGGCTGACTT 50
 17 eValGlyTyrLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
 |||||||||:|||||
 51 TGTAGGCTATAGCTGAGGACAGAGGTTATGCTGTGTGAGCTGGGCTG 100
 34 lYgUGlYpRoaAlaAspProLeuHISglnAlaMetArgAlaAlaGly 50
 |||||||||:|||||
 101 GGGAAAGCCCAAGCCGCGCTGACCAAGCATGGGCGCTGCGA 150
 51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaG 67
 |||||||||:|||||
 151 GACGAGTTGAGACCCGTTTCCGCGCACCTTCTGACCTGGCGGCTCA 200

67 nLeuHISValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
 |||||||||:|||||
 201 GCTACAGTGACCCCAAGGCTCAGCCACGACGCTTCAACAGGTTTCCG 250
 84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
 |||||||||:|||||
 251 ACGAAGCTTTCACAAAGGGGCCCTTAAGTGGGGCGCTGTGTGGCATTTT 300
 101 ValPheGlyValAlaLeuCysAlaGlnGlnSerValAsnLysGlnMetGluPr 117
 |||||||||:|||||
 301 GTCTTTGGGGCTGCCCTGTGTCTGAGAGTGTCAACAAAGAAATGAGACC 350
 117 oLeuValGlyGlnValGlnGlnLysTrpMetValAlaTyrLeuGlnThrArgL 134
 |||||||||:|||||
 351 TTTGGTGGGACAAATCCAGAGATTGATGATGCTGGCTGAGACAGCTC 400
 134 eAlaAspTrpLysSerSerGlyGlyTyrPheAlaGluPheThrAlaLeu 150
 |||||||||:|||||
 401 TGGCTGACTGATCCACAGCAAGTGGGCTGGGCGGACTTCACAGCTCTA 450
 151 TyrGlyAspGlyAlaLeuGlnGlnLysAlaArgArgLeuArgGlnGlyAsnTr 167
 |||||||||:|||||
 451 TACGGGAGACGGGGCCCTGAGAGACGACAGCGCTGTGGGAGAGGCAACTG 500
 167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
 ||| |||:|||||
 501 GGCATGAGTGAACACAGTGTGACGGGGCGCTGGCTGGGCGGCTGG 550
 184 aLThrValGlyAlaPhePheAlaSerLys 193
 |||||||||:|||||
 551 TAAGTGTAGGGGCGCTTTTGTCTAGCAAG 579

seq_name: /SDSL/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:AA25135

seq_documentation_block:

ID AAX25135 standard; DNA; 581 BP.

XX AAX25135;

AC 05-JUL-1999 (first entry)

DT Mouse bcl-w gene derivative.

DE Spermatoogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;

KW animal model; ss.

XX Mus sp.

OS Key

XX CDS

XX W09913710-A1.

XX 25-MAR-1999.

XX 16-SEP-1998; 98WO-A000764.

XX 16-SEP-1997; 97AU-0009228.

XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

XX Adams J, Cory S, Gibson L, Koentgen F, Print C;

XX WPI; 1999-243890/20.

XX P-PSDB; AAY05533.

XX An animal model exhibiting reduced levels of a Bcl-w protein and/or

XX protein associated with Bcl-w

XX Disclosure; Page 38; 52pp; English.

XX The present sequence is described as a derivative of the mouse


```

184  alttttvaalgllyalaphhephalaserlys 193
      |||||
551  ttaactgtatggggcccttttttcttaccagac 579

seq_name: /SIDS1/9c3ddata/geneseq/geneseqn-emb1/NA1998.DAT:AAV41925

seq_documentation_block:
ID  AAV41925 standard; cdna; 1098 BP.
XX
XX  AAV41925;
XX
AC
XX  20-NOV-1998 (first entry)
DT
XX
DE  Nucleotide sequence of the CDNA clone Bcl-1like (HAICH29).
XX
XX  Bcl-1like (HAICH29): chronic inflammatory disease; allergic reaction;
XX  Immunological disorder; autoimmune disease; anti-infectious agent; ss
XX  immunoglobulin

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key	location/Qualifiers
FT	1..1098
FT	/*tag= a
FT	/product= "Bcl-1ike (HAICH29) protein"

PN WO9831800-A2

PD 23-004 1990:
XX

PF	21-JAN-1996;	96MC-0000000.
XX	21-JAN-1997;	97US-0034205.
PR	21-JAN-1997;	97US-0034204.

XX (AUCK-) AUCKLAND UNISERVICES LTD.
PA PA (HUMA-) HUMAN GENOME SCI INC.
PA
YY

XX	1000-414000/25	
PI	Feng P, Gentz RL, Krissansen GW, Ni J, Rosen CA	
PI	Su JY;	

DR New isolated polynucleotides and encoded polypeptides
DR P-PSDB; AAW59884.
XX
PT

PT develop products for treating e.g. autoimmune diseases
PT infections, immunological disorders, autoimmune diseases
PT or tumours
XX

PS	Claim 2; Fig 12A-12D; 120pp; English.
XX	
CC	This is the nucleotide sequence of the cDNA clone Bcl
CC	used in the method of the invention. The products of

used for treating conditions associated with abnormal the polypeptides. They can be used for e.g. treating inflammatory diseases, immunological disorders, autoallergies, and as anti-infective agents.

Sequence 1098 BP; 264 A; 279 C; 325 G; 230 T; 0 other

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alignment_scores: 766.00 Length: 144
Quality: 2
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alignment block:

Ratio:	5.319	gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

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US-09-155-327E-7 x AAV41925      ..
Align seg 1/1   to: AAV41925   from: 1   to: 1098

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1 MetalaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAsp

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|||||
1  ATGGGAGCCCGCCGCTCGCCAGACACAGCGGCTCTGTGTCACACTT 50
17  eValGlYTrLyLeuArGInLySGlYrVaLcYlSGlYAlaGlyPrGc 34
51  TGTAGGTATTAAGCTGAGGCAAGAGGTTATGCTGTGAGGCTGGCCCG 100
34  lYglUGlYPrOAlaAlaAsPProLeuHISglNaLmeArGaLaagly 50
101  GGGAGGGCCCGAGCTGAGCCCGCTGCACCAACGCTTGGGGCAGCTGSA 150
51  AsPluPheGlunThrArgPheArGaArgThrPheSerAsPLeuAlaLaGl 67
151  GATGAGTTCGAGACCCGCTTCGGCCGACCTTCTCTGATCTGGCGGCTCA 200
67  nLeuHISValThrProGlySerAlaGlnGlnArPheThrGlnValaSerA 84
201  GCTGCATGTGACCCCGAGGCTGACGCCACACAGACGCTTACCCAGGCTCCG 250
84  spGlunLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValaLaPhePhe 100
251  ATTAACCTTTTCAAGGGGGGCCCCAACCTGGGGCCGCTGTACCTTCTTT 300
101  ValPheGlYAlaAlaLeuCySaLaGluSerValaLysGluMeGlunPr 117
301  GTCTTGGGGGCTGCACCTGTGTCTGAGAGTCAACAAGAGATGGAAC 350
117  OlauValGlYGlInValGlnGluTrpMetValaLaTrLeuGluThrArgL 134
351  ACTGGGGGCAAGATGACAGAGTGAATGATGTGGCTTACTGGAGACGGCGC 400
134  eUAlaAsPTrPLeHISserSerGlyYTrp 144
401  TGGCTACTGATCCACAGCACTGGGGGCTGG 432

seq_name: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV59630
seq_documentation_block:
ID  AAV59630 standard; DNA; 1864 BP.
XX
AC  AAV59630;
XX
DT  19-JAN-1999 (first entry)
XX
DE  Human secreted protein gene 120 clone HGBGZ64.
XX
KW  Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW  diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW  developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW  immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW  inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW  cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW  osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW  endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS  Homo sapiens.
XX
PN  WO9839448-A2.
XX
PD  11-SEP-1998.
XX
PF  06-MAR-1998; 98WO-US04493.
XX
PR  02-OCT-1997; 97US-0061060.
PR  07-MAR-1997; 97US-0038621.
PR  07-MAR-1997; 97US-0040161.
PR  07-MAR-1997; 97US-0040162.
PR  07-MAR-1997; 97US-0040163.
PR  07-MAR-1997; 97US-0040333.
PR  07-MAR-1997; 97US-0040334.
PR  07-MAR-1997; 97US-0040336.
PR  07-MAR-1997; 97US-0040626.
PR  11-APR-1997; 97US-0043311.

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PR  11-APR-1997; 97US-0043312.
PR  11-APR-1997; 97US-0043313.
PR  11-APR-1997; 97US-0043314.
PR  11-APR-1997; 97US-0043568.
PR  11-APR-1997; 97US-0043569.
PR  11-APR-1997; 97US-0043576.
PR  11-APR-1997; 97US-0043578.
PR  11-APR-1997; 97US-0043580.
PR  11-APR-1997; 97US-0043669.
PR  11-APR-1997; 97US-0043670.
PR  11-APR-1997; 97US-0043671.
PR  11-APR-1997; 97US-0043672.
PR  11-APR-1997; 97US-0043674.
PR  23-MAY-1997; 97US-0047492.
PR  23-MAY-1997; 97US-0047500.
PR  23-MAY-1997; 97US-0047501.
PR  23-MAY-1997; 97US-0047502.
PR  23-MAY-1997; 97US-0047503.
PR  23-MAY-1997; 97US-0047581.
PR  23-MAY-1997; 97US-0047582.
PR  23-MAY-1997; 97US-0047583.
PR  23-MAY-1997; 97US-0047584.
PR  23-MAY-1997; 97US-0047585.
PR  23-MAY-1997; 97US-0047586.
PR  23-MAY-1997; 97US-0047587.
PR  23-MAY-1997; 97US-0047588.
PR  23-MAY-1997; 97US-0047589.
PR  23-MAY-1997; 97US-0047590.
PR  23-MAY-1997; 97US-0047592.
PR  23-MAY-1997; 97US-0047593.
PR  23-MAY-1997; 97US-0047594.
PR  23-MAY-1997; 97US-0047595.
PR  23-MAY-1997; 97US-0047596.
PR  23-MAY-1997; 97US-0047597.
PR  23-MAY-1997; 97US-0047598.
PR  23-MAY-1997; 97US-0047599.
PR  23-MAY-1997; 97US-0047600.
PR  23-MAY-1997; 97US-0047601.
PR  23-MAY-1997; 97US-0047612.
PR  23-MAY-1997; 97US-0047613.
PR  23-MAY-1997; 97US-0047614.
PR  23-MAY-1997; 97US-0047615.
PR  23-MAY-1997; 97US-0047617.
PR  23-MAY-1997; 97US-0047618.
PR  23-MAY-1997; 97US-0047632.
PR  23-MAY-1997; 97US-0047633.
PR  06-JUN-1997; 97US-0048964.
PR  13-JUN-1997; 97US-0048974.
PR  08-JUL-1997; 97US-0049610.
PR  16-JUL-1997; 97US-0051926.
PR  18-AUG-1997; 97US-0052874.
PR  22-AUG-1997; 97US-0055724.
PR  22-AUG-1997; 97US-0056630.
PR  22-AUG-1997; 97US-0056631.
PR  22-AUG-1997; 97US-0056632.
PR  22-AUG-1997; 97US-0056636.
PR  22-AUG-1997; 97US-0056637.
PR  22-AUG-1997; 97US-0056662.
PR  22-AUG-1997; 97US-0056664.
PR  22-AUG-1997; 97US-0056845.
PR  22-AUG-1997; 97US-0056862.
PR  22-AUG-1997; 97US-0056864.
PR  22-AUG-1997; 97US-0056872.
PR  22-AUG-1997; 97US-0056874.
PR  22-AUG-1997; 97US-0056875.
PR  22-AUG-1997; 97US-0056876.
PR  22-AUG-1997; 97US-0056877.
PR  22-AUG-1997; 97US-0056878.
PR  22-AUG-1997; 97US-0056879.
PR  22-AUG-1997; 97US-0056880.
PR  22-AUG-1997; 97US-0056881.
PR  22-AUG-1997; 97US-0056882.
PR  22-AUG-1997; 97US-0056884.

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PR 22-AUG-1997; 97US-0056886.
PR 22-AUG-1997; 97US-0056887.
PR 22-AUG-1997; 97US-0056888.
PR 22-AUG-1997; 97US-0056889.
PR 22-AUG-1997; 97US-0056892.
PR 22-AUG-1997; 97US-0056893.
PR 22-AUG-1997; 97US-0056894.
PR 22-AUG-1997; 97US-0056903.
PR 22-AUG-1997; 97US-0056908.
PR 22-AUG-1997; 97US-0056909.
PR 22-AUG-1997; 97US-0056910.
PR 22-AUG-1997; 97US-0056911.
PR 05-SEP-1997; 97US-0057650.
PR 05-SEP-1997; 97US-0057659.
PR 05-SEP-1997; 97US-0057761.
PR 12-SEP-1997; 97US-0058785.

(HUMA-) HUMAN GENOME SCT INC.

XX PA Bednarik DP, Brewer LA, Carter KC, Duan R, Edner R, Endress GA;
PI Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS;
PI Kyaw H, Lafleur DM, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;
PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;

XX WPI: 1998-506364/43.
DR P-PSDB: AAW74848.

XX New isolated human genes and the secreted polypeptide(s) they encode
PT - useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders

XX Claim 1: Page 353-354; 721pp: English.

XX This sequence represents a nucleic acid molecule designated Gene 120
CC from the human cDNA clone HBG264 (deposited as clone ATCC 97902 and
CC ATCC 200048) which encodes a secreted human protein. The gene can be
CC used to generate fusion proteins by linking to the gene to a human
CC immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of
CC the fused protein as compared to the human protein only.
CC The invention relates to 186 novel genes and their fragments (nucleic
CC acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 186
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAV59511 for described uses).

XX Sequence 1864 BP; 494 A; 403 C; 506 G; 455 T; 6 other;

alignment_scores:
Quality: 766.00 Length: 144
Ratio: 5.319 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment block:

US-09-155-327E-7 x AAV59630 ..

Align seg 1/1 to: AAV59630 from: 1 to: 1864

1 MetAlaThrProAlaSerAlaProAspThrArGAlaLeuValAlaAspH 17
11 ATGGCGACCCGACCGCTGGCCGACACAGCGCTGCTGGCGACACTT 60
17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
61 TGTAGGCTTATTAAGCTGAGCGAGAAAGGTTATGCTGTGGAGCTGGCCCG 110
34 IyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArGAlaAlaGly 50
111 GGGAGGGCCGACGAGCTGACCGCGCTGACACCAAGCCATGGGGGAGCKGGA 160

51 AspGluPheGluThrArGpPheArGThrPheSerAspLeuAlaAlaG 67
161 GATGAGTTGAGACCCGCTTCCGGCAGCACTTCTCTATCTGGGGCTCA 210
67 nLeuHisValThrProGlySerAlaGlnAlaArGpPheThGlnValSerA 84
211 GCTGATGTGACCCGACGCTGACCCAAACAGCTTACCAGCTCCGCG 260
84 sPGLuLeuPheGlnGlyLysProAsnTrpGlyArGLeuValAlaPhePhe 100
261 ATGAACCTTTTCAGGGGGCCCAACTGGGCGCGCTGTGAGCTTCTTT 310
101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluP 117
311 GTCTTGGGGCTGCGACTGTGCTGTAGAGTGTCAACAGAGATGAGAAC 360
117 OLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArG 134
361 ACTGGTGGGACAAAGTGCAGAGTGTGATGTGCTTACTTGGAGAGCGGC 410
134 eValAspTrpIleHisSerSerGlyGlyTyr 144
411 TGGCTGACTGATCCACAGCACTGGGGGCTCG 442

seq_name: /SIDS1/gcdata/geneseq/geneseq-nemb1/NA2002.DAT:ABJ32228

seq_documentation_block:
ID ABJ32228 standard; DNA; 6049 BP.

AC ABJ32228;

DT 26-MAR-2002 (first entry)

XX Human immune system associated gene SEQ ID NO: 201.

XX Human; immune system disease; cytosine methylation; antiasthmatic;
XX antiarteriosclerotic; antihaemic; cytosolic; nototropic;
XX neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
XX antirheumatic; antiarthritic; antidiabetic; antiporiatic;
XX antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
XX acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
XX neurofibromatosis; rheumatoid arthritis; poriasis; bowel disease;
KW gene; ds.

OS Homo sapiens.

PN W0200200928-A2.

XX 03-JAN-2002.

PF 02-JUL-2001; 2001WO-EP07537.

PR 30-JUN-2000; 2000DE-1032529.

PR 01-SEP-2000; 2000DE-1043826.

XX (EPIC-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

DR WPI: 2002-130909/17.

PT Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation

PS Claim 1: SEQ ID NO 201; 32pp + Sequence Listing; German.

XX The present invention provides a number of human immune system associated
XX genes which are modified by the methylation of cytosines. The sequences
XX can be used in the diagnosis and treatment of immune system disorders,
XX including eye diseases such as retinopathy, neovascular glaucoma and
XX macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid

CC Leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
 CC Rheumatoid arthritis, psoriasis and inflammatory/alicerative bowel
 CC diseases. The present sequence is a gene of the invention.
 XX
 SQ Sequence 6049 BP; 1480 A; 109 C; 1549 G; 2911 T; 0 other;

alignment_scores:
 Quality: 444.00 Length: 144
 Ratio: 3.795 Gaps: 0
 Percent Similarity: 81.250 Percent Identity: 65.278

alignment_block:
 US-09-155-327e-7 x ABL32228 ..

Align seg 1/1 to: ABL32228 from: 1 to: 6049

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5001 ATGGCATTTTACTTTCGGTTTACATATACGGTTTGGTGGTGGATT 5050
17 eValGlyTyrLysLeuArgLysGlyTyrValCysGlyAlaGlyProG 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
5051 TGTAGGTATATAGTTAGGTAGAGGTTATGTTGTGAGTTGGTTTCG 5100
34 lYlGlylProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
5101 GGGAGGTTTATAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAG 5150
51 AspGluPheGluThrArgPheArgThrPheSerAspLeuAlaAlaG 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
5151 GATGAGTTGAGATTCGTTTGGCGGTATTTTGGATTGGCGGTTTA 5200
67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
5201 GTTGTATGAGATTATTAAGTTTAAACGTTTAAATTAAGTTTTCG 5250
84 SPGLnLeuPheGlnGlylProAsnTrpGlyArgLeuValAlaPhePhe 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
5251 ATGATTTTATTAAGCGGCTTTAATTGGCGTTCGTTGTGATGTTT 5300
101 ValPheGlyAlaAlaLeuCysAlaGlnSerValAsnLysGlnMetGluPr 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
5301 GTTGTGGGGTGTATCTGTCTGTAGAGTGTATATAGAGATGAGATT 5350
117 OleuValGlylGlnGlnGlylProMetValAlaTyrLeuGlnThrArgL 134
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5351 ATGCGTGGGATTAAGTGTAGAGTGGATGCGTTTATTTGAGACGTA 5400
134 euAlaAspTrpPLeuHisSerSerGlyGlyTrp 144
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seq_name: /SIDS1/gcgdata/geneseq/geneseq-nmb1/NA2001A.DAT:AA500247

seq_documentation_block:

ID AA500247 standard; DNA: 1236 BP.

AC AA500247;

DT 31-MAY-2001 (first entry)

DE Bcl-XL-DTR apoptosis-modifying fusion protein, DNA sequence.

KW Human; Bcl-XL-DTR; apoptosis; cancer; spinal muscular atrophy; ds;

KW diptheria toxin receptor binding domain; DTR; neoplasm; tumour;

KW hyper-proliferation; Alzheimer's disease; neurodegenerative disorder;

KW transient ischaemic neuronal injury; stroke; spinal cord injury;

KW Huntington's disease.

OS Chimeric - Homo sapiens.

OS Chimeric - Corynebacterium diptheriae.

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XX key Location/Qualifiers
FH CDS 1..1236
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FT /product= "Bcl-XL-DTR fusion protein"
FT /note= "DTR is diptheria toxin receptor binding domain"
FT 7..36
FT /*tag= b
FT /note= "10x Histidine tag"
FT 61..759
FT /*tag= c
FT /note= "Bcl-XL gene from codon 1-233"
FT 760..777
FT /*tag= d
FT /note= "linker DNA, linking Bcl-XL to DTR"
FT 778..1236
FT /*tag= e
FT /note= "DTR, diptheria toxin receptor binding domain"
XX WO200112661-A2.
XX
XX PD 22-FEB-2001.
XX
XX PF 15-AUG-2000; 2000WO-US22293.
XX
XX PR 16-AUG-1999; 99US-0149220.
XX
XX PA (HARD ) HARVARD COLLEGE.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Youle RJ, Liu X, Collier RJ;
XX
XX DR MPI; 2001-218343/22.
XX DR P-PSDB; AAU00219.
XX
XX PT Novel fusion protein for modifying apoptosis in target cell and
XX PT reducing apoptosis after transient ischemic neuronal injury, has two
XX PT domains which targets protein to a cell and modifies apoptotic response
XX PT of cell
XX
XX PS Claim 5; Page 54-56; 65pp; English.
XX
XX CC The sequence represents the coding sequence of Bcl-XL-DTR apoptosis-
XX CC modifying fusion protein comprising human Bcl-XL sequence fused via a
XX CC short linker to diptheria toxin receptor binding domain (DTR). The
XX CC functional apoptosis-modifying fusion protein is capable of binding a
XX CC target cell and integrating into or crossing a cellular membrane of the
XX CC target cell. The apoptosis-modifying fusion protein comprises at least
XX CC two domains: the DTR domain, which targets the fusion protein to the
XX CC target cell and the Bcl-XL domain, which modifies an apoptotic response
XX CC (inhibiting or enhancing) apoptosis in a target cell, for modifying
XX CC lymphocyte, cancer, neoplasm, macrophage, epithelial, stem, tumour or
XX CC hyper-proliferative cell or an adipocyte. It is also useful for reducing
XX CC apoptosis in a subject after transient ischemic neuronal injury,
XX CC especially spinal cord injury. The fusion protein may be used to treat
XX CC various diseases and injury conditions through inhibition or enhancement
XX CC of apoptotic cellular response, including neurodegenerative disorders
XX CC such as Alzheimer's disease, Huntington's disease, spinal muscular
XX CC atrophy, stroke episodes and unregulated cell growth as in tumours and
XX CC various cancers. The apoptosis-modifying fusion protein can be delivered
XX CC effectively throughout the body and targeted to selective tissue and
XX CC cells.
XX
XX SQ Sequence 1236 BP; 317 A; 291 C; 343 G; 285 T; 0 other;
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alignment_scores:

Quality: 433.50 Length: 233
 Ratio: 2.949 Gaps: 4
 Percent Similarity: 63.090 Percent Identity: 39.914

alignment_block:


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316 AGTACCTGACATCCAGCTCCACATCACCCAGGAGACATATATCAGAG 365
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78 gPheThrGlnValSerAspGlnLeupheGlnGlyProAsnTrpGlyA 95
|||||.....|
366 CTTTGAACAGGTAGTGAATGAACTCTCCGGATGGGTTAACTGGGGTC 415
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95 rLeuValAlaPhePheValPheGlyAlaAlaLeucysAlaGlnSerVal 111
|||||.....|
416 GCATTTGGCCCTTTTCTCCTTCGGGGGCGACTGTGCGTGAAGCGTA 465
|||||.....|
112 AsnLysGlnMetGlnProLeuValGlyGlnValGlnGlnIuTrpMetValAl 128
|||||.....|
466 GACACAGAGATGCAGGTATTGTGATCGGATCGACCTTGATGCCAC 515
|||||.....|
128 aTyrLeuGlnThrArgLeuAlaAspTrpIleHisSerSerGlyGlyTrpA 145
|||||.....|
516 TTACCTGAATGACCACTAGAGCCTTGATCCAGAGAACGGCGCTGGG 565
|||||.....|
145 LagIupheThrAlaLeuTyrGlyAspGlyAlaLeuGlnGlnAlaArgArg 161
|||||.....|
566 ATACTTTTGGAACTCTATGGAGACATGCAACCGAGAGCCGAAG 615
|||||.....|
162 LeuArgGlu.....GlyAsnTrpAlaSerValArgThrValLeuThrGln 176
|||||.....|
616 GGCACAGAAAGCGCTTCAACCGCTGTCTCAGCGGATGATGCTGGCCGG 665
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176 yAlaValAlaLeuGlyAlaLeu 183
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666 CGTGGTTCTGTGGCTCACTC 687
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OM of: US-09-155-327E-7 to: GenEmbl.* out_format : pfs
 Date: Jun 6, 2002 2:30 PM

About: Results were produced by the GenCore software, version 4.5,
 Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

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 -DB=genembi -OFMT=fastap -SUFFIX=p2n.rge -GAPOP=12.000
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 -DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -NO_XLPHY -WAIT -THREADS=1

Search information block:

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 Query length: 193
 Database: GenEmbl.*
 Database sequences: 1797656
 Database length: 187333701
 Search time (sec): 2386.420000

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gb.pr:BD021198	+ 1007.00	1539.23	2.3e-77	1437	1 BC021198 Homo sapiens, BCL2-11
gb.pr:BD7461	+ 1007.00	1531.90	5.8e-77	3542	1 D87461 Human mRNA for KIAA0271
gb.pat:AR020780	+ 1002.00	1538.93	3.5e-77	579	1 AR020780 Sequence 2 from patent
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gb.pat:MX022529	+ 1000.00	1535.80	3.5e-77	583	1 AX022529 Sequence 6 from patent
gb.pat:MX030817	+ 1000.00	1535.80	3.5e-77	583	1 AX030817 Sequence 6 from patent
gb.to:AR030769	+ 1000.00	1521.30	2.2e-76	3476	1 AF030769 Mus musculus BCL-W (B
gb.pat:AR020779	+ 996.00	1529.72	7.6e-77	579	1 AR020779 Sequence 1 from patent
gb.to:AR096291	+ 965.00	1529.68	7.7e-77	582	1 AR096291 Rattus norvegicus Bcl
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gb.hg:AC084240	+ 670.00	982.53	2.3e-46	181282	1 AC084240 Rattus norvegicus c
gb.to:XR1	+ 646.50	991.03	7.7e-47	749	1 X82462 X.laevi RI mRNA, 7/1997
gb.pat:AX345130	+ 444.00	663.16	1.4e-28	6049	1 AX345130 Sequence 201 from Pat
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gb.pat:BD006625	+ 428.50	649.47	8.2e-28	1742	1 BD006625 A mutagenized rat bcl
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gb.pat:ES2357 + 428.50 637.76 3.7e-27 7372 1 E2357 Virus vector system
 gb.to:RNCBXLX + 424.50 641.33 2.3e-27 2232 1 X82537 R.norvegicus bcl-x g
 gb.to:RN010579 + 420.50 643.88 1.7e-27 764 1 U10579 Rattus norvegicus Bcl
 gb.com:BN092434 + 416.50 638.60 3.3e-27 687 1 U92434 Bos taurus bcl-2 mRNA
 gb.ov:GDPCKBCL2 + 414.00 625.21 1.0e-26 2228 1 Z11961 G.domesticus mRNA fo

seq_name: gb.pr:HSU59747

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 DEFINITION Human Bcl-w (bcl-w) mRNA, complete cds.
 ACCESSION U59747
 VERSION U59747.1 GI:1572492
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 582)
 Gibson,L., Holmgren,S.P., Huang,D.C., Bernard,O., Copeland,N.G.,
 Jenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S.
 bcl-w, a novel member of the bcl-2 family, promotes cell survival
 Oncogene 13 (4), 665-675 (1996)

TITLE

Oncogene 13 (4), 665-675 (1996)

JOURNAL

Oncogene 13 (4), 665-675 (1996)

MEDLINE

REFERENCE

AUTHORS

FEATURES

source

gene

CDS

BASE COUNT

ORIGIN

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Percent Similarity:

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from: 1

to: 582

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151 GATAGTTCGAGACCGCTTCGCGCGACCTCTGATCTGGCGGCTCA 200
67 nleuHISValThrProGlySerAlaGlnGlnAArgPheThrGlnValSera 84
201 GCTCCATGTGACCCGACGCTCAGCCACGACGCTTCACCCAGGTCCG 250
84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
251 ACGACATTTTCAAGGGGGGCCCACTGGGGCGGCTTACCTTCTT 300
101 ValPheGlyAlaAlaLeuGlnGlnSerValAlaGlnGlnMetGluPr 117
301 GTCTTTGGGGCTGCACTGTGTGTGTGAGAGTGTCAACAGAGATGAAAC 350
117 olauValGlyGlnValGlnGlnTrpMetValAlaTyrLeuGlnTrpArgL 134
351 ACTGTGGGAGCAAGTGCAGAGTGTGATGTGCTTACCTGGAGAGCGGC 400
134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
401 TGCTGACAGTGATCCACAGCATGGGGGCTGGCGAGTTCCACAGCTCTA 450
151 TyrGlyAspGlyAlaLeuGlnGlnAlaArgArgLeuArgGlnGlyAsnTr 167
451 TACGGGGAGGGGGCGCTGGAGAGGCGCGGCTGCGGGAGGGGAACCTG 500
167 PalaseValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
501 GGATCATGAGGAGAGACAGTGTGACGGGGCGGCTGGAGCTGGGGCCCTG 550
184 a1ThValGlyAlaPhePheAlaSerIys 193
551 TAACTGTAGGGGCGCTTTTGTCTAGCAAG 579

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seq_name: gb-pr:BC021198

seq_documentation_block:

LOCUS BC021198 1437 bp mRNA linear PRI 22-JAN-2002

DEFINITION Homo sapiens, BC12-like 2, clone MGC:10675 IMAGE:5944307, mRNA,

ACCESSION BC021198 complete cds.

VERSION BC021198.1 GI:18203706

KEYWORDS MGC.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 1437)

Strausberg,R.

Submitted (14-JAN-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: http://mgc.ncl.nih.gov

Contact: MGC help desk

Email: c9apbs-remail.nih.gov

Tissue Procurement: DCTD/DTF

CDNA Library Preparation: Rubin Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)

Sequencing Center (NISC),

Gaithersburg, Maryland:

Web site: http://www.nisc.nih.gov/

Contact: nisc_mgc@nsl.nih.gov

Shevchenko, Y., Wetherby, R.D., Beckstrom-Sternberg, S.M.,

Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,

Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,

REMARK

REFERENCE
AUTHORS
TITLE
JOURNAL

Lim, M., Maduro, O. L., Masello, C., Mastrian, S. D., McCloskey, J. C., McDowell, J. Pearson, R., Snyder, B., Stantitrop, S., Thomas, P. J., Tjongson, E. E., Touchman, J. W., Tsurgeon, C., Vogt, J. L., Walker, M. A., Zhang, L., H. and Green, E. D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov> Series: RAWL Plate: 15 Row: k Column: 19 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14574571.

FEATURES
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/lab_host="DH10B-R"
/notes="Vector: pOTB7"
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/db_xref="GI:18203707"
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AMAAADDEFETRRFTSDLAQLVHTPEASOORTOVSDELFOGPGWAGLVAFV
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BASE COUNT
ORIGIN

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303 a 343 c 509 g 282 t

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Ratio: 5.218 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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US-09-155-327e-7 x BC021198 ..

Align seg 1/1 to: BC021198 from: 1 to: 1437

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17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
226 TGTAGGTTATTAAGCTGAGCGAGAGGTTATGCTGTGAGCTGGCCCG 275
34 lylGlnGlyProAlaAlaAspProLeuHISGlnAlaMetArgAlaGly 50
276 GGGAGGGGCCAGCAGCTGACCCAGCTGCACCAACGATGGGGCAGCTGA 325
51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAla1a1 67
326 GATGAGTTCGAGACCGCTTCGCGGCGACCTCTGTGATCTGGCGGCTCA 375
67 nleuHISValThrProGlySerAlaGlnGlnAArgPheThrGlnValSera 84
376 GCTGCTGTGACCCGACGCTCAGCCACACMACGCTTCAACCCAGGCTCCG 425
84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
426 ATGAACTTTTCAAGGGGGGCCCACTGGGGCGGCTTGTGACCTTCTT 475
101 ValPheGlyAlaAlaLeuGlnGlnSerValAlaGlnGlnMetGluPr 117
476 GTCTTTGGGGCTGCACTGTGTGTGTGAGAGTGTCAACAGAGATGAAAC 525
117 olauValGlyGlnValGlnGlnTrpMetValAlaTyrLeuGlnTrpArgL 134

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526 ACTGTGGGACAAGTCAGAGTGTGCTGCTACTGAGACCGGC 575
 134 euAlaasprtrpIleHisSerSerGlyTTPAlaGluPheThrAlaLeu 150
 576 TGGCTGCTGATGCACACAGTGGGGCTGGCGAGTTCACACTCTTA 625
 151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
 626 TACGGGACGGGGCCCTGGAGAGGGCGCTGGCGGAGGAGACTG 675
 167 palAservaIargThrValIeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
 676 GGCATCAGTGAAGACAGTCTGACGGGGCCGCGCATGGGGCCCTGG 725
 184 alThrValGlyAlaPhePheAlaSerLys 193
 726 TAACTGTAGGGCCCTTTTGTCTAGCAAG 754

seq_name: gb_pr.D87461

seq_documentation_block:

LOCUS D87461 3542 bp mRNA linear PRI 06-OCT-2001

DEFINITION Human mRNA for KIAA0271 gene, complete cds.

ACCESSION D87461

VERSION D87461.1 GI:1944417

KEYWORDS KIAA0271.

SOURCE Homo sapiens male brain myoblast cell_line:KG-1 cDNA to mRNA, clone.lib:PSPT 1 clone:HA6752.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 3542)

AUTHORS Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawarabayashi,Y., Ohara,O., Tanaka,A., Kotani,H., Miyajima,N. and Nomura,N.

TITLE Prediction of the coding sequences of unidentified human genes. VI. The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of cDNA clones from cell line KG-1 and brain

JOURNAL DNA Res. 3 (5), 321-329 (1996)

MEDLINE 97191544

2 (bases 1 to 3542)

REFERENCE Ohara,O., Nagase,T., Kikuno,R. and Nomura,N.

AUTHORS Direct Submission

TITLE Submitted (27-AUG-1996) Osamu Ohara, Kazusa DNA Research Institute; 1532-3, Yata, Kisarazu, Chiba 292-0812, Japan

JOURNAL (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)

FEATURES

source

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/clone="HA6752"

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BASE COUNT 804 a 817 c 1030 g 891 t

ORIGIN

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 Ratio: 5.218 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

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US-09-155-327e-7 x D87461 ..

Align seg 1/1 to: D87461 from: 1 to: 3542

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17 euAlaGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34

227 TGTAGCTTATAGCTGAGGACGAGAGGTTATGCTGTGGAGCTGGCCCG 276

34 LysGlyLysProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50

277 GGGAGGCCCGACAGCTGAGCCCTGACACCAACCCATGGCGGAGCTGGA 326

51 AspGluPheGluThrArgPheArgThrPheSerAspLeuAlaAlaG 67

327 GATGAGTTCGAGACCCGCTTCCGGCGACCTTCTGATCTGGCGGCTCA 376

67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84

377 GCTCATGTGACCCACAGCTCAGCCCAACACCTTCACCCAGCTCTCG 426

84 spGluLeuPheGlnGlyLysProAsprThrArgLeuValAlaPhePhe 100

427 ATGAACCTTTTCAAGGGGGCCCAACTGGGGCCGCTTGTAGCTCTTT 476

101 ValPheGlyAlaAlaLeuGlyAlaGlnLysValAsnLysGluMetGluP 117

477 GTCTTGGGGCTGCACGTGTGTGAGAGTGTCAACAAGAGATGAGAAC 526

117 OLeuValGlyGlnValGlnGluThrPheMetValAlaTyrLeuGluThrArg 134

527 ACTGGTGGACAGACAGTGCAGATGTGGCTTACTGTGAGAGCGCGGC 576

134 euAlaAsprtrpIleHisSerSerGlyTTPAlaGluPheThrAlaLeu 150

577 TGGCTGATGATCCACAGCATGTGGGGCTGGCGAGTTACAGCTCTTA 626

151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167

627 TACGGGACGGGGCCCTGGAGAGCGCGGCTGCGGGAGGGAAGCTG 676

167 palAservaIargThrValIeuThrGlyAlaValAlaLeuGlyAlaLeuV 184

677 GGCATCAGTGAAGACAGTGTGACGGGGCCGTGGCACTGGGGGCCCTGG 726

184 alThrValGlyAlaPhePheAlaSerLys 193

727 TAACTGTAGGGCCCTTTTGTCTAGCAAG 755

seq_name: gb_pat:AR020780

seq_documentation_block:

LOCUS AR020780 579 bp DNA linear PAT 05-DEC-1998

DEFINITION Sequence 2 from patent US 5789201.

ACCESSION AR020780

VERSION AR020780.1 GI:3975395

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

1 (bases 1 to 579)

Genes coding for bcl-2 and bcl-2 homologue

Patent: US 5789201-A 2 04-AUG-1998;

Location/Qualifiers

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  Ratio: 5.219          Gaps: 0
  Percent Similarity: 99.482  Percent Identity: 99.482
alignment_block:
  US-09-155-327e-7 x AR020780 ..
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  |||||||
51 TGTAGCTTAAAGCTGACGACAGAGGCTTATGCTGTGAGCTGCGCCG 100
34 lYgLuGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
  |||||||
101 GGGAGGGGCCGACGAGCTGACCCACCAAGCCATGCGGGGACGCTGGA 150
51 AspGluPheGluThrArgPheArgThrPheSerAspLeuAlaAlaGly 67
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151 GATGAGCTTGAGACCCGCTCCGCGCACCTTCTGTGATCGCGGCTCA 200
67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSera 84
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117 cLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
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151 TyrGlyAspGlyAlaLeuGluGlnAlaArgArgLeuArgGluGlyAsnTr 167
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551 TAACTGAGGGGCGCTTTTGTGACAGAG 579
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seq_documentation_block:
LOCUS          MM059746          582 bp      mRNA      linear      ROD 29-SEP-1996
DEFINITION     Mus musculus Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION      U59746
VERSION        059746.1  GI:1572494
KEYWORDS
SOURCE          house mouse.

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ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 582)
AUTHORS
Gibson, L., Holmgreen, S. P., Huang, D. C., Bernard, O., Copeland, N. G.,
Jenkins, N. A., Sutherland, G. R., Baker, E., Adams, J. M. and Cory, S.
JOURNAL
Oncogene 13 (4), 665-675 (1996)
MEDLINE
96358615
REFERENCE
2 (bases 1 to 582)
AUTHORS
Gibson, L., Holmgreen, S. P., Huang, D. C. S., Bernard, O., Adams, J. M. and
Cory, S.
TITLE
Direct Submission
JOURNAL
Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and
Eliza Hall Institute of Medical Research, PO Royal Melbourne
Hospital, Parkville, Victoria 3050, Australia
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  Ratio: 5.181          Gaps: 0
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67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSera 84
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84 sPGLuLeuPheGlnGlnGlyLysProAsnTrpGlyArgLeuValAlaPhePhe 100
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301 gcttttggggcgcctctgtgctcagactgcacaaacaaatggagcc 350
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351 tttagtgagcaagatgcagagatggatgctggcctacctgagacacagtc 400
134 euliasprrplienhserserctgyltyrpalagiuphetthalaleu 150
401 tggctgactgctgagatccacacaaattggggcctggcggagattcacagctca 450
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451 tagcgggacggcgcccttgagagacacggcgcttgcggaggggaactcg 500
167 palaservalargthrvalleuthrghiyalavalaleucliyaleuy 184
501 ggcactcagtgagacagctcctacacggggcgctggcactgggggcccctgg 550
184 althrvvalglialaphpealaserlys 193
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seq_documentation_block:

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ACCESSION	AX030817				
VERSION	AX030817.1	GI:10278311			
KEYWORDS					
SOURCE	. unidentified.				
ORGANISM	. unidentified.				
REFERENCE	1 (bases 1 to 583)				
AUTHORS	Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.				
TITLE	A novel mammalian gene, bcl-1w, belongs to the bcl-2 family of apoptosis-controlling genes				
JOURNAL	Patent: WO 9735971-A 6 02-OCT-1997;				
	ADAMS JERRY MCEE (AU) ; HOLMGREEN SHAUN P (AU) ; CORY SUZANNE (AU) ; GIBSON LEONIE M (AU) ; ANRAD OPERATIONS PTY LTD (AU)				
location/Qualifiers	1..583				

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Ratio:	5.181	Gaps:		0
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 1 ATGGCGACCCCGACCTCGGCCCCACACACACGGGCTCTGGTGGCAGACTT 5
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FEATURES
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gene
CDS

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BASE COUNT      111 a      157 c      200 g      114 t
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Ratio: 5.161 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 98.446

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Align seg 1/1 to: AF096291 from: 1 to: 582

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51 TGTAGCTATAGCTGAGCAGCAAGGGTTATGCTGTGGAGCTGCCCTG 100
34 LysGlyGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
101 GGGAGGCCCGACAGCCGACCCGCTGCACCAAGCATGCGGAGCGTGA 150
51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaGly 67
151 GACGAGTTTGAGACCCGCTGCCGACACTTCTCTACCTGGCCGCTCA 200
67 nLeuHisValThrProGlySerAlaGlnAlaArgPheThrGlnValSer 84
201 GCTACAGCTGACCCAGGCTCAGCCAGCAACGCTTCACCCAGGTTCCG 250
84 spGluLeuPheGlnGlyGlyProAsnThrPGLyArgLeuValAlaPhe 100
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101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGlu 117
301 GTCTTTGGGCTGCGCTGTGCTGAGAGTGTCAACAAGAAATGAGCC 350
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351 ATTGGTGGACAAAGTGCAGGATTGATGTGACCTACCTGGAGACACGCT 400
134 euAlaAspThrLeuHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
401 TGGCTGACGATCCACAGCAGTGGGGCTGGGGGAGATTCACAGCTCTA 450
151 TyrGlyAspGlyAlaLeuGluGlnAlaArgArgLeuArgGluGlyAsn 167
451 TACGGGACCGGGCCCTGGAGAGCGACGCGTTCGGGAGGAGACG 500
167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeu 184
501 GGCATGAGTGAAGACAGTGTGACGGGGCGTGTGGCAGCTGGGGCCCTG 550

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184 aThrValGlyAlaPhePheAlaSerLys 193
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seq_name: gb_pat:AX022531

seq_documentation_block:

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LOCUS      AX022531          581 bp      DNA      linear      PAT 07-SEP-2000
DEFINITION Sequence 8 from Patent EP0932674.
ACCESSION  AX022531
VERSION     AX022531.1  GI:10046127
KEYWORDS
SOURCE      unidentified.
ORGANISM    unidentified.
REFERENCE   1 (bases 1 to 581)
AUTHORS     Adams,J.M., Holmgren,S.P., Cory,S. and Gibson,L.M.
TITLE       A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
JOURNAL     apoptosis-controlling genes
PATENT      Patent: EP 0932674-A 8 04-AUG-1999;
FEATURES
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CDS

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BASE COUNT 105 a 164 c 195 g 117 t
ORIGIN

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Percent Similarity: 98.446 Percent Identity: 94.819

alignment_block:

US-09-155-327E-7 x AX022531 ..

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51 TGTAGCTATAGCTGAGCAGCAAGGGTTATGCTGTGGAGCTGCCCTG 100
34 LysGlyGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
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51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaGly 67
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67 nLeuHisValThrProGlySerAlaGlnAlaArgPheThrGlnValSer 84
201 GCTACAGCTGACCCAGGCTCAGCCAGCAAGCATTCACCCAGGTTCCG 250
84 spGluLeuPheGlnGlyGlyProAsnThrPGLyArgLeuValAlaPhe 100
251 ACGAACTTTTCCAAAGGGGGCCCACTGGGGCGCTGTGGCAGCTGGGGCCCTG 300

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101 ValPheGlyAlaAlaLeuGlyAlaGlySerValAlaGlyGluMetGluPr 117
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301 GTCTTTGGGGCTGCTGCTGCTGAGAGTGTCAACAAGAAATGAGGCC 350
117 OLeuValGlyGlnValGlnGluTrpMetValAlaGlyTrpGluThrArgL 134
351 TTTGGTGGGACAAAGTCCAGATTGGATGCTGCTGCTGAGACACAGTC 400
134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
401 TGGCTGACTGATCCACAGCAGTGGCGGCTGGCGGAGCTTCAACAGCTCA 450
151 TyrGlyAspGlyAlaLeuGlnGluAlaAlaArgArgLeuArgGluGlySnr 167
451 TACGGGGAGCGGGCCCTGGAGAGCAGCGCGTCTGGCGGAGGAGCAACTG 500
167 PalaservAlaArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeu 184
501 GGCAATGAGTGAACAGTGTGACGGGGGCGGCTGGCACTGGGGGCGCTGG 550
184 alThrValGlyAlaPhePheAlaSerLys 193
551 TAACTGTAGGGGCTTTTTCCTAGCAAG 579

seq_name: gb_pat:AX030819

seq_documentation_block:
LOCUS AX030819 581 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 8 from Patent WO9735971.
ACCESSION AX030819
VERSION AX030819.1 GI:10278313
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 581)
AUTHORS Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.
TITLE A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
JOURNAL apoptosis-controlling genes
ADAMS JERRY MCKEE (AU) ; HOLMGREEN SHAUN P (AU) ; CORY SUZANNE (AU)
; GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)
FEATURES
source
1..581
location/Qualifiers
1..581
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/db_xref="taxon:32644"
1..507
/note="unnamed protein product"
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/db_xref="GI:10278314"
/translation="MPTPASTPPTTRAIIVADFGVRLRKGVCAGGPGEGPADPLHQ
AMRAAGDEFFERFRRTSDLAQILHTVPSAQRFTQYDNLFGCGPMGRIVAFYF
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RLREGNNA"
BASE COUNT 105 a 164 c 195 g 117 t
ORIGIN
alignment_scores:
Quality: 965.00 Length: 193
Ratio: 5.079 Gaps: 0
Percent Similarity: 98.446 Percent Identity: 94.819

alignment_block:
US-09-155-327E-7 x AX030819 ..
Align seq 1/1 to: AX030819 from: 1 to: 581
1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspH 17
117 OLeuValGlyGlnValGlnGluTrpMetValAlaGlyTrpGluThrArgL 134
1 ATGCGACACCCAGCGCTCAACCCAGACACACGCGCTCTAGTGGCTGACTT 50

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17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
51 TGTAGGCTRTAGCTGAGGAGCAAGGTTATGTCTGTGAGACTGGGCTG 100
34 IyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
101 GGAAGAGCCAGCCCGCCGACCGCTGACACAAAGCCATCGGGGCTGTGA 150
51 AspGluPheGluThrArgPheArgArgTrpPheSerAspLeuAlaAlaG 67
151 GACGAGTTTGAACCCGTTTCCGCCGACCTTCTGTGACTGGCGGCTCA 200
67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSera 84
201 GCTACACGTCGACCCAGCGTCAAGCCAGCAACGCTTCAACCCAGTTCCG 250
84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
251 ACGAATCTTTCACAAAGGGGCGCTTAACCTGGGGCGCTTGTGCAATCTT 300
101 ValPheGlyAlaAlaLeuGlyAlaGlySerValAlaGlyGluMetGluPr 117
301 GTCTTTGGGGCTGCTGCTGCTGAGAGTGTCAACAAGAAATGAGGCC 350
117 OLeuValGlyGlnValGlnGluTrpMetValAlaGlyTrpGluThrArgL 134
351 TTTGGTGGGACAAAGTCCAGATTGGATGCTGCTGAGACACAGTC 400
134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
401 TGGCTGACTGATCCACAGCAGTGGCGGCTGGCGGAGCTTCAACAGCTCA 450
151 TyrGlyAspGlyAlaLeuGlnGluAlaAlaArgArgLeuArgGluGlySnr 167
451 TACGGGAGCGGGGCGCTGGAGAGCAGCGCGTCTGGCGGAGGAGCAACTG 500
167 PalaservAlaArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeu 184
501 GGCAATGAGTGAACAGTGTGACGGGGGCGGCTGGCACTGGGGGCGCTGG 550
184 alThrValGlyAlaPhePheAlaSerLys 193
551 TAACTGTAGGGGCTTTTTCCTAGCAAG 579

seq_name: gb_pr:CNS0000B
seq_documentation_block:
LOCUS CNS0000B 196292 bp DNA linear PRI 22-MAY-2001
DEFINITION Human chromosome 14 DNA sequence BAC R-124D2 of library RPCI-11
from chromosome 14 of Homo sapiens (Human), complete sequence.
ACCESSION AL049829
VERSION AL049829.4 GI:8217859
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 196292)
Heilig,R., Petit,J.L., Vico,Y., Dasilva,C., Robert,C., Wincker,P.,
Brottier,P., Cattolico,L., Barde,V., Pelletier,E., Artiguenave,F.,
Levy,M., Eckenberg,R., Bruls,T., Deberardinis,V., Cruaud,C.,
Gyapay,G., Saurin,W. and Weissenbach,J.
Sequencing of the human chromosome 14
Unpublished
2 (bases 1 to 196292)
Genoscope.
Direct Submission
Submitted (21-MAY-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
On Jun 3, 2000 this sequence version replaced gi:5138746.
----- Genome Center
Center: Genoscope / Centre National de Sequencage

```

Center code: GS
Web site: <http://www.genoscope.cns.fr/>
Contact: Segref@genoscope.cns.fr

The following BAC sequence is oriented from the T7 to the SP6 end.
Upstream BAC (overlapping the T7 end) : R-244E17
Downstream BAC (overlapping the SP6 end) : C-2201G16 (AC=AL132855)

Summary Statistics
Assembly program: Phrap; version 2.0
Quality coverage: 7.94x in Q20 bases; sum-of-contigs

Overall quality chart :

```

Range : bases
0
1 - 9
10 - 19
20 - 29
30 - 39
40 - 49
50 - 59
60 - 69
70 - 79
80 - 89
90 - 99
111256

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Percentage of bases with a quality value >= 40 : 99 %.

Location/Qualifiers

1. 196292

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="14"

/clone_id="RPC1-11"

78259. 78398

/note="matching EMBL:AA908790

RHdb:RH102162

dbSTS:STS69699

Identified using the e-PCR software (G. Schuler)"

80433. 80566

/note="matching EMBL:AA167748

RHdb:RH98727

dbSTS:STS68485

Identified using the e-PCR software (G. Schuler)"

82164. 82299

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RHdb:RH78773

dbSTS:STS55514

Identified using the e-PCR software (G. Schuler)"

93580. 93808

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RHdb:RH75103

dbSTS:STS52191

Identified using the e-PCR software (G. Schuler)"

107758. 107951

/note="matching EMBL:R94929

RHdb:RH65111

dbSTS:STS45044

Identified using the e-PCR software (G. Schuler)"

107996. 108181

/note="matching EMBL:DL1677

RHdb:RH47139

dbSTS:STS40201

Identified using the e-PCR software (G. Schuler)"

128387. 128525

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RHdb:RH53520

dbSTS:STS25817

Identified using the e-PCR software (G. Schuler)"

128419. 128543

/note="matching EMBL:R87257

RHdb:RH53698

dbSTS:STS18321

STS Identified using the e-PCR software (G. Schuler)"

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dbSTS:STS42930

Identified using the e-PCR software (G. Schuler)"

138509. 138658

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dbSTS:STS24710

Identified using the e-PCR software (G. Schuler)"

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dbSTS:STS20162

Identified using the e-PCR software (G. Schuler)"

138568. 138677

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RHdb:RH28671

dbSTS:STS20163

Identified using the e-PCR software (G. Schuler)"

138805. 138926

/note="matching EMBL:H72023

RHdb:RH68657

dbSTS:STS48564

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161617. 161761

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RHdb:RH92419

dbSTS:STS65422

Identified using the e-PCR software (G. Schuler)"

194804. 194903

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RHdb:RH76320

dbSTS:STS53407

Identified using the e-PCR software (G. Schuler)"

BASE COUNT 50870 a 45673 c 47123 g 52626 t

ORIGIN

1

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Quality: 873.50 Length: 399

Ratio: 4.526 Gaps: 2

Percent Similarity: 48.371 Percent Identity: 47.870

alignment_block:

US-09-155-327e-7 x CNS000B ..

Align seg 1/1 to: CNS000B from: 1 to: 196292

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17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34

89876 TGTAGCTTATAAGCTGAGCAGAGGGTTATGTCGTGGAGCTGGCCCC 89925

34 LysGlnGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50

89926 GGGAGGGCCACGACGCTGACCCGTCGACCAAGCCATCGGGCAGCTGCA 89975

51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaG 67

89976 GATGAATTGGACACCCGCTTCGGCGCCACCTTCTGTGATGGCGGCTCA 90025

67 nLeuHisValThrProGlySerAlaGlnAlaArgPheThrGlnValSer 84

90026 GCTGCATGTGACCCAGGCTCAGCCACAGCGCTTACACAGGCTCTCG 90075

84 spGluLeuPheGlnGlyProAsnTrpGlyArgLeuValAlaPhePhe 100

90076 ATGACCTTTTTCAGGGGGCCCCCACTGGGGCCCTTGTAGCTTCTT 90125
 101 ValPheGlyAlaLeuCysAlaGluSerValAlaAspGluMetGluPr 117
 90126 GTCTTGGGGCTGCTGCTGTCTGCTGAGAGTGTCAACAGAGATGGAACC 90175
 117 OleuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluTrpArgL 134
 90176 ACTGTGGGACAGAGTGTGAGAGTGTGGCTTACCTGAGACGACAGC 90225
 134 eulaAspTrpIleHisSerGlyGlyTrp..... 144
 90226 TGGCTGCTGGATCCACAGCAGTGGGGCTGGTAAAGAGCTTTCATTT 90275
 144 144
 90276 GCGGCTGACACATCTTTCACAAAGCTGTCTCCAGGGGAGATGGG 90325
 144 144
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 144 144
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 145 Ala 145
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 146 GluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArgArgL 162
 90876 GGAGTTCACAGCTCTATACGGGAGCGGGCCCTGGAGAGCGCGCGCTC 90925
 162 euaArgGluGlyAsnTrpAlaSerValArgThrValLeuThrArgAlaVal 178
 90926 TCCGGAGGAGGAGACTGGGCATCTGAGGACAGTGTGAGGGGGCGCTG 90975
 179 AlaLeuGlyAlaLeuValThrValGlyAlaPhePheAlaSerIlys 193
 90976 GCATGGGGGCGCTGTACTGTAGGGGCTTTTCTCTAGCAAG 91020

seq_name: gb_hly:AC079885

seq_documentation_block:

LOCUS AC079885 151212 bp DNA linear HTG 08-NOV-2000

DEFINITION Rattus norvegicus chromosome 4 clone RP31-246H18 strain Brown

ACCESSION AC079885

VERSION AC079885.2 GI:11120768

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

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REFERENCE

AUTHORS

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JOURNAL

REFERENCE

AUTHORS

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JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

FEATURES

source

NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 20440: contig of 20440 bp in length
 20441 20540: gap of unknown length
 20541 41009: contig of 20469 bp in length
 41010 41109: gap of unknown length
 41110 65552: contig of 24443 bp in length
 65553 110365: gap of unknown length
 65553 110365: contig of 44713 bp in length
 110366 110465: gap of unknown length
 110466 151212: contig of 40747 bp in length.

Location/Qualifiers
 1. 151212
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 /strain="Brown Norway"
 /db_xref="taxon:10116"

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vector_side:left
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65653..110365
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  Ratio: 4.012        Gaps: 1
  Percent Similarity: 86.528      Percent Identity: 69.430

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US-09-155-327E-7 x AC079885 ..

Align seg 1/1 to: AC079885 from: 1 to: 151212

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|||||.....|
74605 .....GCTGGCCCGG 74614
34  LysGlyLysProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
|||||.....|
74615 GGGAGAGCCCAACACAGCCACCTGATACCCACCATGCGGCTGCTGGA 74664
51  AspGluPheGluThrArgPheArgThrPheSerAspLeuAlaAlaGly 67
|||||.....|
74665 GACAAAGTTAGAGACCACTCCAGCACCTCTGACCTGCCACTCA 74714
67  nLeuHisValThrProGlySerAlaGlnAlaArgPheThrGlnValSera 84
|||||.....|
74715 GCTACATGTGATGCCAGGCTCAGCCCAACAAAGCTTCAACCCAGGTTCCA 74764
84  spGluLeuPheGlnGlyLysProAsnTyrGlyArgLeuValAlaPhePhe 100
|||||.....|
74765 ACGAACTTTCCAAAGGGGGCCCACTAGGCGCATCTGTACATCTTT 74814
101 ValPheGlyAlaAlaLeuGlyAlaGlnSerValAlaGlnGluMetGluPr 117
|||||.....|
74815 GCTCTTGGGGGCTGCTGTGCTGAGAGTCAACAAATAATAGAGCC 74864
117  oLeuValGlyLysValGlnGluTyrPheValAlaTyrLeuGlnThrArgL 134
|||||.....|
74865 ATTGGTGGGACAAAGTCAGATGTGATGCTGCTACCCAGACAGCC 74914
134  eValAspTyrPheHisSerSerGlyTyrPalaGluPheThrAlaLeu 150
|||||.....|
74915 TGGGCTGATGATCCACAAATGGGGCTGCTGAGTTCCACAGCTCTA 74964
151  TyrGlyAspGlyAlaLeuGlnGluAlaArgArgLeuArgGluGlnGlySnr 167
|||||.....|
74965 TTCCGATGGGGCCCTTAGAAGACATGCTGTGAGGAGGAGGAGCTG 75014
167  PalSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeu 184
|||||.....|

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75015 GGCATCAGTGGAGCAATAGTACTGGGGCTGTGACACTGGGAGCCCTCA 75064
184  aLthrValGlyAlaPhePheAlaSerLys 193
|||||.....|
75065 TAACTGTAAAGGCGCTTTTACTAACAAG 75093
seq_name: gb_hlg.AC084240

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DEFINITION Rattus norvegicus chromosome 4 clone RP31-103121 strain Brown
ACCESSION  AC084240
VERSION    AC084240.1 GI:10864175
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE     Norway rat.
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
1 (bases 1 to 181282)
Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W.,
Bouffard, G.G., Brinkley, C., Dietrich, N.L., Gupta, J., Ho, S.-L.,
Idol, J., Lee-Lin, S.-O., Legaspi, R., Lim, M., Maduro, Q. L.,
Maduro, V.B., Mastrian, S.D., McCloskey, J.C., McDowell, J.,
Pearson, R., Prasad, A., Snyder, B., Stantiprop, S., Thomas, J.W.,
Thomas, P.J., Tjongson, E.E., Touchman, J.W., Tran, J.T., Tsurgon, C.,
Vogt, J.L., Walker, M.A., Wetherby, K.D. and Green, E.D.
Unpublished
NISC Mouse Sequencing Initiative
2 (bases 1 to 181282)
Green, E.D.
Direct Submission
Submitted (18-OCT-2000) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
----- Project Information
Center project name: r1
Center clone name: 103121
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 179798 bases at least Q40
Consensus quality: 180132 bases at least Q30
Consensus quality: 180274 bases at least Q20
Insert size: 138000; agarose-fp
Insert size: 160000; sum-of-contigs
Insert size: 180982; sum-of-contigs
Quality coverage: 15.02x in Q20 bases; agarose-fp
Quality coverage: 12.95x in Q20 bases; pulse-field-gel
Quality coverage: 11.45x in Q20 bases; sum-of-contigs

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NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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1 5430: contig of 5430 bp in length
* 5431 5530: gap of unknown length
* 5531 39503: contig of 33973 bp in length
* 39504 39603: gap of unknown length
* 39604 85792: contig of 46189 bp in length
* 85793 85892: gap of unknown length
* 85893 181282: contig of 95390 bp in length.
Location/Qualifiers

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FEATURES

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                1. 5430
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                clone_end:Sp6
                vector_side:right"
                5531. 39503
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                vector_side:left"
                39604. 85792
                /note="assembly_fragment"
                85893. 181282
                /note="assembly_fragment"
BASE COUNT      50811 a 36290 c 37296 g 56560 t      325 others
ORIGIN
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alignment_scores:
    quality: 670.00      Length: 193
    Ratio: 4.012        Gaps: 1
    Percent Similarity: 86.528    Percent Identity: 69.430
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alignment_block:

US-09-155-327e-7 x AC084240 ..

Align seg 1/1 to: AC084240 from: 1 to: 181282

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17 eValGIyTrLysLeuArgInLysGIyTrValCySGIyAlaGIyProG 34
|||||.....|
49829 .....GCTGGCCCCG 49838
34 IyGIuGIyProAlaAlaAspProLeuHisGIuAlaMetArgAlaAlaGIy 50
|||||.....|
49839 GGAAGGCCCAACAGCAACCTGATACACCAAGCCATGGGCTGCTGGA 49888
51 AspGIuPheGIuThrArgPheArgArgThrPheSerAspLeuAlaAlaGI 67
|||||.....|
49889 GACAAAGTTAGAGACCCACTTCCAGCACACCTTCTGTGACCTGGCCACTCA 49938
67 nLeuHisValThrProGIySerAlaGIuInArgPheThrGIuAlaSerA 84
|||||.....|
49939 GCTACATGTGATGCCAGGCTCAGCCCAACAATGCTTCAOCCAGTTTCCA 49988
84 spGIuLeuPheGIuInGIyGIyProAsnTrPGIyArgLeuValAlaPhePhe 100
:::|||||.....|
49989 ACGAACTTTTCCAAAGGGGCCCACTAGGGCCACTTGTGACATTCTTT 50038
101 ValPheGIyAlaAlaLeuCysAlaGIuSerValaAsnLysGIuMetGIuPr 117
|||||.....|
50039 GTCCTTGGGGCTGCCCTGTGTGTGAGTGTCAACAGAAATAGAGGCC 50088
117 oLeuValGIyGIuInGIuGIuTrPheValAlaLaTrGIyLeuGIuThrArgL 134
|||||.....|
50089 ATTGGTGGGAGCAAGTGCAGATGTGATGGCTTACCCAGAGACAGGCC 50138
134 euAlaAspTrPIeHisSerGIyGIyTrAlaGIuPheThrAlaLeu 150
|||||.....|
50139 TGGCTGACTGGATCCACAATGGGGCTGGGTGAGTTACAGCTCTTA 50188
151 TyrGIyAspGIyAlaLeuGIuInGIuAlaArgArgLeuArgGIuGIyAsnTr 167
:::|||||.....|
50189 TTCGGAAATGGGCCCTTAGAAGAGACATGTGTGTAGGAGGAGGAGCTG 50238
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167 pAlaSerValArgThrValLeuThrGIyAlaValAlaLeuGIyAlaLeuV 184
|||||.....|
50239 GGCATCAGTGGAGACAAATACTGTGGGCTGTGACACTGGGAGCCCTGA 50288
184 alThrValGIyAlaPhePheAlaSerLys 193
:::|||||.....|
50289 TAACTGTAAAGGCCCTTTTACTTAACAAG 50317
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 6, 2002, 11:57:05 ; Search time 66.15 Seconds
(without alignments)
2161.129 Million cell updates/sec

Title: US-09-155-327E-8
Perfect score: 582
Sequence: 1 atggcgagccagccagctcaac.....ccttttttctagcaagtga 582

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : Issued Patents, NA: *
1: /cgcn2_6/prodata/1/ina/5A.COMB.seq: *
2: /cgcn2_6/prodata/1/ina/5B.COMB.seq: *
3: /cgcn2_6/prodata/1/ina/6A.COMB.seq: *
4: /cgcn2_6/prodata/1/ina/6B.COMB.seq: *
5: /cgcn2_6/prodata/1/ina/PCROS.COMB.seq: *
6: /cgcn2_6/prodata/1/ina/Backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	558.2	95.9	579	1 US-08-798-897-1	Sequence 1, Appl
2	558.2	95.9	579	2 US-08-978-523-1	Sequence 1, Appl
3	515	88.5	579	1 US-08-798-897-2	Sequence 2, Appl
4	515	88.5	579	2 US-08-978-523-2	Sequence 5, Appl
5	134.6	23.1	926	2 US-08-081-448-5	Sequence 6, Appl
6	134.6	23.1	926	2 US-08-470-670A-6	Sequence 1, Appl
7	134.6	23.1	926	4 US-08-481-739-1	Sequence 1, Appl
8	134.6	23.1	926	4 US-09-167-921-1	Sequence 39, Appl
9	134.6	23.1	926	4 US-09-277-020-39	Sequence 1, Appl
10	134.6	23.1	926	4 US-09-323-743-1	Sequence 6, Appl
11	134.6	23.1	926	4 US-08-461-511A-6	Sequence 1, Appl
12	134.6	23.1	926	5 US-08-461-511A-6	Sequence 6, Appl
13	134.6	20.9	717	2 US-08-465-485A-20	Sequence 20, Appl
14	121.8	20.9	1274	2 US-09-080-285-20	Sequence 1, Appl
15	121.8	20.9	1274	2 US-08-470-670A-1	Sequence 1, Appl
16	121.8	20.9	1274	4 US-08-461-511A-1	Sequence 1, Appl
17	121.8	20.9	1274	5 PCT-US94-07089-1	Sequence 1, Appl
18	121.8	20.9	1303	1 US-08-081-448-1	Sequence 1, Appl
19	121.8	20.9	4825	6 5459251-1	Patent No. 5459251
20	121.8	20.9	5086	2 US-08-465-485A-19	Sequence 19, Appl
21	121.8	20.9	5086	2 US-08-365-486A-14	Sequence 14, Appl
22	121.8	20.9	5086	3 US-09-080-285-19	Sequence 19, Appl
23	121.8	20.9	5086	4 US-08-880-342-14	Sequence 14, Appl
24	121.8	20.9	5086	5 PCT-US93-05651-4	Sequence 4, Appl
25	121.8	20.9	5086	5 PCT-US93-06251-2	Sequence 2, Appl
26	121.8	20.9	5094	4 US-09-234-186-7	Sequence 7, Appl
27	121.8	20.9	5104	6 5506344-1	Patent No. 5506344

28	120.2	20.7	760	1 US-08-405-702A-11	Sequence 11, Appl
29	120.2	20.7	1846	2 US-08-365-486A-16	Sequence 16, Appl
30	120.2	20.7	1846	4 US-08-880-342-16	Sequence 16, Appl
31	117.4	20.2	615	2 US-08-465-485A-22	Sequence 22, Appl
32	117.4	20.2	615	3 US-09-080-285-22	Sequence 22, Appl
33	117.4	20.2	911	4 US-09-126-109-5	Sequence 5, Appl
34	117.4	20.2	911	5 PCT-US93-06251-3	Sequence 3, Appl
35	114.2	19.6	831	6 5459251-3	Patent No. 5459251
36	114.2	19.6	831	6 5506344-4	Patent No. 5506344
37	73.2	12.6	623	6 5506344-3	Patent No. 5506344
38	57	9.8	737	1 US-08-081-448-7	Sequence 7, Appl
39	57	9.8	737	2 US-08-470-670A-8	Sequence 8, Appl
40	57	9.8	737	4 US-08-461-511A-8	Sequence 8, Appl
41	57	9.8	737	5 PCT-US94-07089-8	Sequence 8, Appl
42	47.6	8.2	5408	1 US-08-471-058-20	Sequence 20, Appl
43	47.6	8.2	5408	1 US-08-471-057-20	Sequence 20, Appl
44	40.8	7.0	1287	1 US-08-471-058-8	Sequence 8, Appl
45	40.8	7.0	1287	2 US-08-944-530-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-798-897-1
Sequence 1, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmund, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ. ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
US-08-798-897-1

Query Match 95.9%; Score 558.2; DB 1; Length 579;
Best Local Similarity 97.8%; Pred. No. 2.3e-143;
Matches 566; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 1 atggcgagccagccagctcaacacagcgagcttagtgagctgtagctat 60
DB 1 atggcgagccagccagctcaacacagcgagcttagtgagctgtagctat 60

QY	61	aagctcgaaagcaaaaggtatctctgtgtgaaagcttgggaaagccaaagcccgagc	120
Db	61	AAGCTGAAGACAAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAAGGCCACAGCCGCAC	120
QY	121	ccgctgcaccaaagccatgcgggctgtgtgaaagcagttttagaacccgtttccgcgcacc	180
Db	121	CCGCTGCACCAAGCCATCGGGCAGCTGGAACACAGTTTGAGACCCGCTTCCGGCGCAC	180
QY	181	ttctctgaacctggccgcacagctcaacgctgaccccaagctcagcccaagcgtttacc	240
Db	181	TTCTCTGACCTGGCCGCTCAGCTTACAGCTGACCCAGAGCTAGCCCAAGACGTTTCACC	240
QY	241	caggtttccagcaaatctttccaaaggggcccctaactgtgggcgctctgtgcatcttt	300
Db	241	CAGGTTTCCGACGAACCTTTCCAAAGGGGGCCCCAACGTGGGGCCGTGTTGGCATCTTT	300
QY	301	gtctttggggcttgcgcccctgtgtctgagaggtgtcaacaagaataatggagcctttgtgtgga	360
Db	301	GTCCTTGGGGGCTGCCCTGTGTGCTGTGAAGTGTCAACAAAGAAATGAGCCATTGGTGGGA	360
QY	361	caagtgcagaatcttgatgtgtgcacctactgtgaaacacgctctgtgtgactgataccaaag	420
Db	361	CAAGTGCAGAACTTGATGTGATCTACTTACCTGGAGACAGCTTGGCTGACTGTGATCCACAGC	420
QY	421	agttgcgagcttggggcgagtttcaacgctctataacgggggacggggcccttgagagagcaag	480
Db	421	AGTGGGGGCTGGCGGAGTTTCACAGCTCTATTACGGGGACCGGGGCCCTGGAGGAGGCACGG	480
QY	481	cgtctgcggaggggaaacttgcatacagctagagcaatgtcttgacccggggagccgtgtgaaact	540
Db	481	CGTCTGCGGAGGGGAACCTGGGCACTACGTAGAGACATGCTGTGACGGGGGCTGTGGCACTG	540
QY	541	ggggccctgtgtaactgtgaggggcctttttgtctagcaag	579
Db	541	GGGGCCCTGTGTAAGTGTAGGGGCCCTTTTGTCTAGCAAG	579

RESULT 2
 US-08-978-523-1
 : Sequence 1, Application US/08978523
 : Patent No. 5883229
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Guestella, John
 : TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
 : TITLE OF INVENTION: Homologue
 : NUMBER OF SEQUENCES: 53
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: STERNE, KESLER, GOLDSTEIN & FOX P.L.L.C.
 : STREET: 1100 New York Avenue, N.W., Suite 600
 : CITY: Washington
 : STATE: DC
 :
 : COUNTRY: USA
 :
 : ZIP: 20005
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.30
 :
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/978,523
 : FILING DATE: herewith
 : CLASSIFICATION: 424
 : CLASSIFICATION: 424
 :
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/798,897
 : FILING DATE: February 11, 1997
 : CLASSIFICATION: 424
 :
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Esmond, Robert W.
 : REGISTRATION NUMBER: 32,893
 : REFERENCE/DOCKET NUMBER: 1483.0140002
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 202-371-2500
 : TELEFAX: 202-371-2540

```

? INFORMATION FOR SEQ ID NO: 1
?
? SEQUENCE CHARACTERISTICS:
?
?   LENGTH: 579 base pairs
?   TYPE: nucleic acid
?   STRANDEDNESS: both
?   TOPOLOGY: both
?   MOLECULE TYPE: cDNA
?
US-08-978-523-1

```

Query Match	95.9%	Score 558.2;	DB 2;	Length 579;
Best Local Similarity	97.8%;	Pred. No. 2.3e-143;		
Matches 566; Conservative	0;	Mismatches 13;	Indels 0;	Gaps 0;

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Db	1	ATGGGCAACCCGACCCCTCAACACCCGAGACACACGGGCTCTATGGCTCACTTTATAGGCTAT	60
QY	61	aggctgaagcacaaggtctatgtctgtgtgaagcttgcgcctctgggaagagcccgacgac	120
QY	61	AAGCTAGACACAAGAGGTTATGCTGTGTGAGACTGGCTTGGGAAAGGCCACACACCTCAC	120
Db	121	ccgcttgacccaagccatctgcggcgtctgtgagaaagatttgagaccggtttccgcgcgac	180
QY	121	ccgcttgacccaagccatctgcggcgtctgtgagaaagatttgagaccggtttccgcgcgac	180
Db	121	CCGCTGCACACAAGCCATGCGGGGAGAGCTGGAGAGAGAGTTTGAGACCGCGGTTCGGGGCAC	180
QY	181	ttctctgacctgtgcgcgtcagctctaacgttaaccaggtctcagcccgaaagcttaac	240
QY	181	TTCTCTGACCTTGCGGCTCAAGCTACAGGTACCCAGGCTCAAGCCACACGCTTCAAC	240
Db	241	caagttcccgaaacatttccaaaggggcgcctaaccttgggcgcgtctgtgacattctt	300
QY	241	CAAGTTCCGAGAACCTTTTCAAGGGGGGCCCAACATGGGGCGTCTTG6CAATTCTT	300
Db	301	gaccttggggcgtgcgcctgtgtgtcgtgaagtgtaaaaagaatgtgaaccttgtgtgga	360
QY	301	gaccttggggcgtgcgcctgtgtgtcgtgaagtgtaaaaagaatgtgaaccttgtgtgga	360
Db	301	GTCTTTGGGGGCTGCCCTGTGTGCTGAGAGTGTAACAAAAGAAATGAGACCAATTGTGTGGGA	360
QY	361	caagtgtcagagatgtgatgtgtgccttaccttggagaacagctctgcgtcgtacttgatccagc	420
Db	361	CAAGTGCAGAGATTGGATGGTGACCTACCTGTGAACACAGCTTGCTGACTGGATTCACAGC	420
QY	421	agtgtgcgctgtggcgtgttcaacagctctatacggggaagcgggcctctggaagaagcag	480
QY	421	agtgtgcgctgtggcgtgttcaacagctctatacggggaagcgggcctctggaagaagcag	480
Db	421	AATGGGGGCTGGGCGGAGTTTCAAGCTCTATACGGGAGCGGGCCCTGTGAAGAGCAAGG	480
QY	481	cgctctgcggaggggaaactgtggacatcaatgtgagaaacagtgtctaacgggggcgttgactg	540
QY	481	CGCTCGCGGAGGGAACTGGGCAATCAATGAGAGACAGTCTGTACGGGGGCGTGTGGCACTG	540
Db	541	ggggcctcgtgtaactgttaggggcctttttgtctagcaag	579
QY	541	ggggcctcgtgtaactgttaggggcctttttgtctagcaag	579
Db	541	GGGGCCCTGTGTAAGTGTAGGGGCGCTTTTGTGCTAGCAAG	579

RESULT 3
 US-08-798-897-2
 Sequence 2, Application US/08798897
 Patent No. 5789201
 GENERAL INFORMATION:
 APPLICANT: Guastella, John
 TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
 TITLE OF INVENTION: Homologue
 NUMBER OF SEQUENCES: 53
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNER, KESSLER, GOLDSTEIN & FOX P. L. L.C
 STREET: 1100 New York Avenue, N.W., Suite 600
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483,0140001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-08-798-897-2

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Query Match      88.5%; Score 515; DB 1; Length 579;
Best Local Similarity 93.1%; Pred. No. 1,4e-131;
Matches 539; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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Db
OY 61 agcctgaagcgaagaggtatgtctgtgagcctgagcctgaggaagcccaagccgcag 120
    61 AAGCTGAGGCGAAGAGGTTATGTCTGTGTGAGCTGTGCGCCCGGAGGCGCCAGAGCTGAC 120
Db
OY 121 ccgctgacacaaagcctatgctgtgtgagagaggtttgagagccgcttccgcgcagc 180
    121 CCGCTGACACAAAGCCTATGCTGTGTGAGAGAGGTTTGAAGACCGGCTTCCGCGCAGC 180
Db
OY 181 ttctctgacgtgagcgtcgaacgtacacgtgaccccaagctcaagcccaagcctcaac 240
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OY 361 caagtgcaagatgtagtggctgagcctgagagacagctcgtggtgtgagcttccagc 420
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OY 421 agtggagcgttggcgaaggtacacagctctataagggagcagggcccttgaagagcag 480
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OY 481 cgtctcgagagaggaacttgcagcctcagcctcagcctcagcctcagcctcagcctc 540
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RESULT 4
US-08-978-523-2
; Sequence 2, Application US/08978523
; Patent No. 5883229

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GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483,0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-08-978-523-2

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Query Match      88.5%; Score 515; DB 2; Length 579;
Best Local Similarity 93.1%; Pred. No. 1,4e-131;
Matches 539; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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OY 1 atggcgaaccccaagcctcaaccccaagacacacagcgtctagctgactgtagctat 60
    1 ATGGCGACCCCGAGCTCGCGCCAGACACCGGCTCTGTGTGAAGACTTTGTAGATTAT 60
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OY 61 agcctgaagcgaagaggtatgtctgtgagcctgagcctgaggaagcccaagccgcag 120
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Db
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OY 181 ttctctgacgtgagcgtcgaacgtacacgtgaccccaagctcaagcccaagcctcaac 240
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Db

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OY 481 cgtctgcggagggagcagctgagcagctgagcagctgagcagctgagcagctgagcag 540
481 CGTCTGCGGAGGGGAGACTGGGATCAGTGAAGGACACTGCTGACGGGGCGCTGGCAGTg 540
OY 541 ggggcccgtgtaactgtgagggcctttttgtcagcag 579
|||||
Db 541 GGGGCGCTGTACTGTAGGGGCTTTTGTGTCAGCAAG 579

RESULT 5
US-08-081-448-5
; Sequence 5, Application US/08081448
; Patent No. 5646008
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.
; APPLICANT: Boise, Lawrence H.
; TITLE OF INVENTION: Vertebrate Apoptosis Gene:
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5646008th Clark Street, Suite 800
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/081,448
; FILING DATE: 19930622
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5646008thrup, Thomas E.
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-744-0090
; TELEFAX: 312-755-4489
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..836
; US-08-081-448-5

Query Match 23.1%; Score 134.6; DB 1; Length 926;
Best Local Similarity 58.3%; Pred. No. 8,7e-28;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;
OY 128 accaagcagcggcgtgctgtgagcagcttgaagccgcttcgcccagcacttctctg 187
Db 394 AGCAAGGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 453
OY 188 acctggcggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 247
Db 454 ACCTGAGCATCCGAGCTCCAGCATCACCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 513
OY 248 cgaagcagcacttccaaaggggcccttaactgagggcgctctgtgacatcttcttctt 307

Db 514 TGAATGAACTCTTCCGGGATGGGCTAAACTGGGGGTGCATGTGGCTTTTCTCCTCG 573
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Db 574 GCGGGGCACTGTGCTGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 633
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Db 634 CAGCTTGATGCGCAGCTTACCTGAATCACCCTTAAGGAGGAGGAGGAGGAGGAGGAGGAG 693
OY 428 gctggcggagctacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 487
Db 694 GCTGGATACTTGTGTGAGACTCTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 753
OY 488 ggggagggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 532
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RESULT 6
US-08-470-670A-6
; Sequence 6, Application US/08470670A
; Patent No. 5834309
; Patent No. 5834309 5710045
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.
; APPLICANT: Boise, Lawrence H.
; TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,670A
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,448
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARCD:090--1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..836
; US-08-470-670A-6

Query Match 23.1%; Score 134.6; DB 2; Length 926;
Best Local Similarity 58.3%; Pred. No. 8,7e-28;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;


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QY 128 accaagcatcgaggctgctgagagagatttgagaccggtttccgacacttctc 187
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Db 394 AGCAAGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 453
QY 188 accctggcgcctcagctacagctgagcccaagctcagcccaagctcagccaggtt 247
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Db 454 ACCTGACATCCACACTGCATCATCCACCCAGGAGAGCATATCAGAGCTTTGAACAGT 513
QY 248 ccgagcaactttccaaagggggcccctaactgagggcgctctgtgagcttctgtctt 307
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Db 514 TGAATGAACTCTCCGGGATGGGATGAACCTGGGATGAGCTTTGTCCTTTG 573
QY 308 gggcgccctgtgtgagagtgctcaaaagaatgagaccttggtyggacaagtg 367
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Db 574 GCGGGGCACTGGCTGCGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 633
QY 368 aggattgagtggtgctcactgtagagacagctgctgctgagctatccaaagagtg 427
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Db 634 CAGCTTGATGGCCACTTACCTGATGACCACTAGAGCCTTGATGATCAGAGAGGAGG 693
QY 428 gctggcgagagtgctcagctctatacagggagcgccctgagagagcaagcgctctgc 487
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Db 694 GCTGGGATACCTTTGTGGAACCTCTATGGAGACATGAGAGGAGGAGGAGGAGGAGG 753
QY 488 gggaggggaactggtgcatcagtgagagacagtgtgagagggggcg 532
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Db 754 AGGAACGCTTCAACCGCTGTCTCTGACGGGAGGAGGAGGAGGAGGAGGAGGAGG 798

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RESULT 7
US-08-481-739-1
; Sequence 1, Application US/08481739
; Patent No. 6143291

```

GENERAL INFORMATION:

```

APPLICANT: June, Carl H. and Thompson, Craig B.
TITLE OF INVENTION: METHODS FOR ENHANCING T CELL SURVIVAL
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,739
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,518
FILING DATE: 04-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A. (GAD)
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: RPT-034CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214

```

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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 135..836

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US-08-481-739-1

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Query Match 23.1%; Score 134.6; DB 3; Length 926;
Best Local Similarity 58.3%; Pred. No. 8.7e-28;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

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QY 128 accaagcatcgaggctgctgagagagatttgagaccggtttccgacacttctc 187
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Db 394 AGCAAGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 453
QY 188 accctggcgcctcagctacagctgagcccaagctcagcccaagctcagccaggtt 247
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Db 454 ACCTGACATCCACACTGCATCATCCACCCAGGAGAGCATATCAGAGCTTTGAACAGT 513
QY 248 ccgagcaactttccaaagggggcccctaactgagggcgctctgtgagcttctgtctt 307
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Db 514 TGAATGAACTCTCCGGGATGGGATGAACCTGGGATGAGCTTTGTCCTTTG 573
QY 308 gggcgccctgtgtgagagtgctcaaaagaatgagaccttggtyggacaagtg 367
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Db 574 GCGGGGCACTGGCTGCGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 633
QY 368 aggattgagtggtgctcactgtagagacagctgctgctgagctatccaaagagtg 427
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Db 634 CAGCTTGATGGCCACTTACCTGATGACCACTAGAGCCTTGATGATCAGAGAGGAGG 693
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Db 694 GCTGGGATACCTTTGTGGAACCTCTATGGAGACATGAGAGGAGGAGGAGGAGGAGG 753
QY 488 gggaggggaactggtgcatcagtgagagacagtgtgagagggggcg 532
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Db 754 AGGAACGCTTCAACCGCTGTCTCTGACGGGAGGAGGAGGAGGAGGAGGAGGAGG 798

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RESULT 8

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US-09-167-921-1
; Sequence 1, Application US/09167921A
; Patent No. 6172216

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GENERAL INFORMATION:

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APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett P.
APPLICANT: Nickoloff, Brian J.
APPLICANT: Zhang, QingQing
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
FILE REFERENCE: ISPH-0324
CURRENT APPLICATION NUMBER: US/09/167,921A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 926
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (135)..(836)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: L20121 Genbank
DATABASE ENTRY DATE: 1994-07-26
US-09-167-921-1

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Query Match 23.1%; Score 134.6; DB 4; Length 926;
Best Local Similarity 58.3%; Pred. No. 8.7e-28;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

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QY 128 accaagcatcgaggctgctgagagagatttgagaccggtttccgacacttctc 187
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 394 agcaagcgctgaggaggagcgagcgaggttgagactgctgagcgagcgagtgatcagtg 453

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QY 188 accatgacgtcagctacacgtgacccagcgtccagccagcgttcacacgtttt 247
DB 454 accatgacgtcagctacacgtgacccagcgttcacacgtttt 247
QY 248 ccagcagcgttcacacgtgacccagcgttcacacgttcacacgttcacacgttc 307
DB 514 tgaatgacgttcacacgtgacccagcgttcacacgttcacacgttcacacgttc 307
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DB 574 ggcgtgacgttcacacgtgacccagcgttcacacgttcacacgttcacacgttc 367
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QY 428 gctggagcgttcacacgtgacccagcgttcacacgttcacacgttcacacgttc 487
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RESULT 9
US-09-277-020-39
Sequence 39, Application US/09277020
Patent No. 6210892
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
TITLE OF INVENTION: Alteration of mRNA Processing
FILE REFERENCE: ISPH-0339
CURRENT APPLICATION NUMBER: US/09/277,020
CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 09/167,921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 39
LENGTH: 926
TYPE: DNA
ORGANISM: Homo sapiens
US-09-277-020-39

Query Match 23.1%, Score 134.6; DB 4; Length 926;
Best Local Similarity 58.3%; Pred. No. 8,7e-28;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;
QY 128 accaagcagctgagcgtcgtgagacaggttgagacccgtttccgcgcacacgttc 187
DB 394 agcaagcagctgagcgtcgtgagacaggttgagacccgtttccgcgcacacgttc 187
QY 188 accatgacgttcacacgtgacccagcgttcacacgttcacacgttcacacgttc 247
DB 454 accatgacgttcacacgtgacccagcgttcacacgttcacacgttcacacgttc 247
QY 248 ccagcagcgttcacacgtgacccagcgttcacacgttcacacgttcacacgttc 307
DB 514 tgaatgacgttcacacgtgacccagcgttcacacgttcacacgttcacacgttc 307
QY 308 ggcgtgacgttcacacgtgacccagcgttcacacgttcacacgttcacacgttc 367
DB 574 ggcgtgacgttcacacgtgacccagcgttcacacgttcacacgttcacacgttc 367
QY 368 agatgacgttcacacgtgacccagcgttcacacgttcacacgttcacacgttc 427
DB 634 cagctgacgttcacacgtgacccagcgttcacacgttcacacgttcacacgttc 427
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QY 488 ggcgtgacgttcacacgtgacccagcgttcacacgttcacacgttcacacgttc 532
DB 754 agaacgttcacacgtgacccagcgttcacacgttcacacgttcacacgttc 532

RESULT 10
US-09-323-743-1
Sequence 1, Application US/09323743
Patent No. 6214986
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett P.
APPLICANT: Nickoloff, Brian J.
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
FILE REFERENCE: ISPH-0368
CURRENT APPLICATION NUMBER: US/09/323,743
CURRENT FILING DATE: 1999-06-01
EARLIER APPLICATION NUMBER: 09/277,020
EARLIER FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 09/167,921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 926
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (135)..(836)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: L20121 Genbank
DATABASE ENTRY DATE: 1994-07-26
US-09-323-743-1

Query Match 23.1%, Score 134.6; DB 4; Length 926;
Best Local Similarity 58.3%; Pred. No. 8,7e-28;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;
QY 128 accaagcagctgagcgtcgtgagacaggttgagacccgtttccgcgcacacgttc 187
DB 394 agcaagcagctgagcgtcgtgagacaggttgagacccgtttccgcgcacacgttc 187
QY 188 accatgacgttcacacgtgacccagcgttcacacgttcacacgttcacacgttc 247
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QY 428 gctggagcgttcacacgtgacccagcgttcacacgttcacacgttcacacgttc 487
DB 694 gctggagcgttcacacgtgacccagcgttcacacgttcacacgttcacacgttc 487
QY 488 ggcgtgacgttcacacgtgacccagcgttcacacgttcacacgttcacacgttc 532
DB 754 agaacgttcacacgtgacccagcgttcacacgttcacacgttcacacgttc 532

Thu Jun 6 16:39:25 2002

us-09-155-327e-8.rni

Page 10

GenCore version 4.5
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OW nucleic - nucleic search, using sw model

Run on: June 6, 2002, 11:24:29 ; Search time 2348.74 Seconds
(without alignments)
3344.443 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthm:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl1:*
10: gb_estl2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pin:*
16: em_gss_vtl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	578.8	99.5	3487	11 AK004680	AK004680 Mus muscu
3	496.2	85.3	804	AL157542	AL157542 DKEZ761D
4	495.6	85.2	1030	10 BE793530	BE793530 601590016
5	445	76.5	815	10 BF785386	BF785386 602111728
6	430.6	74.0	697	10 BF770566	BF770566 603060362
7	429.8	73.8	854	11 AK013244	AK013244 Mus muscu
8	417	71.6	792	10 BG298789	BG298789 602396527
9	411.6	70.7	540	9 AM258810	AM258810 um74a02.Y
10	366.8	63.0	643	10 BI910270	BI910270 603069493
11	325.4	55.9	362	9 AA596919	AA596919 v021f08.T
12	286.8	49.3	758	10 BI764428	BI764428 603050701
13	277.4	47.7	749	9 BB856021	BB856021 BB856021
14	254.2	43.7	749	10 BG677345	BG677345 602624059
15	246.8	42.4	601	10 BF204905	BF204905 601866718
16	233.6	40.1	433	9 AM326901	AM326901 20104 MAR
17	214.6	36.9	473	10 BE647090	BE647090 UT-M-BH1-

18	204.6	35.2	601	10 BM191403	BM191403 da186a10.
19	188.6	32.4	612	10 BE508939	BE508939 dc14h09.Y
20	183.4	31.5	447	9 BB851239	BB851239 BB851239
21	182.4	31.3	431	9 AM048567	AM048567 UT-M-BH1-
22	157.4	27.0	416	9 AM159063	AM159063 za50h02.x
23	149.4	25.7	628	12 AO532175	AO532175 RPEC1-11-3
24	146.2	25.1	549	12 AO665088	AO665088 HS-5340_B
25	138.2	23.7	624	9 BE188975	BE188975 db62a05.x
26	137.8	23.7	648	9 AL632408	AL632408 AL632408
27	134.6	23.1	687	10 BE293685	BE293685 601186941
28	133	22.9	455	12 AO401160	AO401160 HS-5062_A
29	132.2	22.7	700	10 BE831301	BE831301 602766132
30	132.2	22.5	699	10 BE870269	BE870269 601447403
31	131.2	22.5	697	10 BI457116	BI457116 603185360
32	131.2	22.5	965	10 BM457276	BM457276 AGENCOURT
33	131.2	22.5	974	10 BE250036	BE250036 600943041
34	128	22.0	913	10 BG244406	BG244406 602356535
35	127.6	21.9	862	10 BG735330	BG735330 602842233
36	126.8	21.8	818	10 BG824757	BG824757 602728745
37	126.8	21.8	890	9 AL537680	AL537680 AL537680
38	126.8	21.8	973	10 BG180671	BG180671 602329448
39	126.2	21.7	808	10 BI222971	BI222971 602943462
40	125.2	21.5	836	10 BM018295	BM018295 603645951
41	122	21.0	630	10 BJ060637	BJ060637 BJ060637
42	121.4	20.9	513	10 BM363392	BM363392 BS320054B
43	121.2	20.8	456	12 AZ537061	AZ537061 AST-2P015
44	120.4	20.7	571	10 BJ041701	BJ041701 BJ041701
45	120.4	20.7	657	10 BJ062464	BJ062464 BJ062464

ALIGNMENTS

RESULT 1	AK015644	1949 bp	mRNA	linear	HTC 19-JAN-2002
LOCUS	AK015644				
DEFINITION	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930488D08:Bcl2-like 2, full insert sequence.				
ACCESSION	AK015644				
VERSION	AK015644.1	GI:12854052			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (strain: C57BL/6J) adult male testis cDNA to mRNA, clone.lib:RIKEN full-length enriched mouse cDNA library				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (sites)				
TITLE	Carninci, P., and Hayashizaki, Y.				
JOURNAL	High-efficiency full-length cDNA cloning				
MEDLINE	Meth. Enzymol. 303, 19-44 (1999)				
PUBMED	99279253				
REFERENCE	10349936				
AUTHORS	2 (sites)				
TITLE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.				
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
MEDLINE	Genome Res. 10 (10), 1617-1630 (2000)				
PUBMED	20499374				
REFERENCE	11042159				
AUTHORS	3 (sites)				
TITLE	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasliwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, Y., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.				
JOURNAL	RIKEN integrated sequence analysis (RISA) system--384-format				
MEDLINE	Genome Res. 10 (11), 1757-1771 (2000)				
PUBMED	20530913				

Db 384 CAGGCTCCGATGAACTTTTTCAGAGGGGCCCACTGGGGCGCCTTGAGCCTTTT 443
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RESULT 5
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 LOCUS 602111728F1 NCI CGAP_Kid14 Mus musculus cDNA clone IMAGE:4239798
 DEFINITION 5', mRNA sequence.

ACCESSION Bf785386
 VERSION Bf785386.1 GI:12090422
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 815)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov
 Plate: LLM853 row: h column: 07
 High quality sequence start: 3
 High quality sequence stop: 650.

FEATURES source

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 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4239798"
 /clone_lib="NCI CGAP_Kid14"
 /lab_host="DH10B (TI phage-resistant)"
 /note="Organ: Kidney; Vector: pCMV-Sport6; Site:1: NotI; Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library. 1"
 BASE COUNT 166 a 212 c 296 g 141 t

Query Match 76.5%; Score 445; DB 10; Length 815;
 Best Local Similarity 96.5%; Pred. No. 3e-99; Indels 9; Gaps 7;
 Matches 530; Conservative 0; Mismatches 10;

QY 21 ccagagacacggccttagtggcgtgactgtgagctatagagctgagagcagaaggtta 80

Db 2 CCAGACACACGGGCTCTAGTGTGAC--TTTGAAGCTATTAACCTGAGCAACAAGGTTA 60
 QY 81 tgtctgtgagctggtccctgggaaagccagccgagccgctgacaaagccatgca 140
 Db 61 TGTCTGTGAGACTTGCCCTGGGGAAGGCCACGCCGCCGACCCCTGACCAAGCCATGGC 120
 QY 141 ggtctgtgagagagcttggagccgcttccgcgcgaccttctctgacctggcgctca 200
 Db 121 GGCTCTGGAACAGAG--TTGAGACCCGCTTCCGCCGACCTTCTGACCTGACCCCTCA 179
 QY 201 gctacagtgaccccaagctcagcccaagcaagcttaccaccaagttccagcaacttt 260
 Db 180 GTTACAGCTGACCCAGGCTCAGCCAGCAAGCTTACCCAGCTTCCAGCAACTTTT 239
 QY 261 ccaagggggcccttaacttggggcgtctgtgtgacattcttctgttgggctgacctg 320
 Db 240 CCAGGGGGCCTTAACTGGGGCGCTTGTGGCAATTCT--TGCTTGGGGCTGCGTGTG 296
 QY 321 tgtctgagagtgtaacaagaatgagaccttgggtgtgagaaagtgcagagattgagtg 380
 Db 297 TGCTGAGAGTGTCAACAAGAAATGAGACC--TTGGTGGGACAGTGTGAGATTGATG 355
 QY 381 ggcctaccctggagagacgtctgtgactgataccacagcagctgctggtggcaggt 440
 Db 356 GCGCTACCTGGAGACAGCTGTGCTGACTGATCCACAGCAAGTGGGGCTGGCGGAGTT 415
 QY 441 caagctctatacggagaggggccccttgagagagcagcgctctggggggggagactg 500
 Db 416 CACAGCTCTATACGGGAGCGGGGCCCTGGAGAGGACACGG--CTCTGGCGGAGGGAGAC-G 473
 QY 501 ggcataagtgagagacagctgtgacggggcgctggcactgtggggccctgtaactgtagg 560
 Db 474 GGCATCAGTGAAGAGACAGTGTGACGGGGGCGCTGGGACCT--GGGGCGCTGTAACTGAG 532
 QY 561 ggcctcttt 569
 Db 533 GGCCTTTT 541

RESULT 6
 B1770566 697 bp mRNA linear EST 25-SEP-2001
 LOCUS 603060362F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5209862 5',
 DEFINITION mRNA sequence.
 ACCESSION B1770566
 VERSION B1770566.1 GI:15762144
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 697)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov
 Plate: LLM1526 row: k column: 15
 High quality sequence start: 21
 High quality sequence stop: 695.

FEATURES source

1. 697
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5209862"

/clone_11b="NIH_MGC_122"
 /lab_host="DH10B"
 /Organ: Organ: pooled lung and spleen; Vector: pCNV-SPORT6;
 Site_1: NotI; Site_2: EcoRV (destroyed); RNA source:
 anonymous pool of 24 week female lung, 16 week female
 spleen, and 20-22 week male spleens. Library is oligo-dT
 primed and directionally cloned (EcoRV site is destroyed
 upon cloning). Average insert size 1.4 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 026. Note:
 this is a NIH_MGC Library."

BASE COUNT 121 a 202 c 248 g 126 t
 ORIGIN

Query Match 74.0% Score 430.6; DB 10; Length 697;
 Best Local Similarity 92.0%; Pred. No. 1e-95; Indels 5; Gaps 5;
 Matches 509; Conservative 0; Mismatches 39;

QY 1 atggcagccaccagcctcaaccacagacacagggcctctagctgctgacttgaagctat 60
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
 Db 145 ATGGCAGCCACCAGCCTCGGCGCCAGACACAGGGGCTCTGGTGGCAGACTTTGAGGTTAT 204
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
 QY 61 agagctggcaggaagggtatgtctgtgagctggccctgggggaagggcccgccgac 120
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
 Db 205 AAGCTGAGCGAGAAAGGTTATGTCTGTGTGGAGCTGGGCCCGGGGAGGGCCACAGCTGAC 264
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
 QY 121 ccgctgacacaaagccatgcggctctgtgagagagtttgaagccgttccgccaac 180
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
 Db 265 CCGCTGACCAACGACATGCGGAGCTGGAGATGATTTGAGAACCCCGCTTCCGGGCGCAC 324
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
 QY 181 ttctctacactggcctcagctacacgctgacccagctcagccagcagcttcaac 240
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
 Db 325 TTCTCTGATGTGCGGCTCACTGCTGATGTGACCCAGGCTCCAGCAACAGCTTTCAC 384
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
 QY 241 caggttccgacgaacttttcaagggggcccttaactggggcgtctgtgcatcttt 300
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
 Db 385 CAGGTCTCCGATGACTTTTTCAGAGGGGCCCACTGGGGCGCCCTGTGACCTTCTTT 444
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
 QY 301 gttcttggggggtgctctgtg-tgcgagaggttcaacaagaatggaagccttggtag 359
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
 Db 445 GTTCTTGGGGGCTGCTGCTGCTGAGTGTCAACAAGAGAGATGAGAACACAGTGGG 504
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
 QY 360 acaagtcagagatgtgatgtgcttact-ggagacagctgtgctgctacagatcaca 418
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
 Db 505 ACAAGTCAGAGATGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 564
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
 QY 419 ggaatggcggtggcgaggttcaagctctatc-ggggaagggggccttgggaagga 477
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
 Db 565 GCAAGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGGACGGGCGCTTGAGAGAGCG 624
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
 QY 478 cggcgtcttgcggggaaggaactggca-tcaagttagagcag-tgctacagggggcgctg 535
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
 Db 625 CGGCGCTTCGCGGAGGAGGAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 684
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
 QY 536 cactggggggcct 548
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
 Db 685 CACTGGGGGCGCT 697

RESULT 7
 LOCUS AK013244 854 bp mRNA linear HTC 19-JAN-2002
 DEFINITION Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
 enriched library, clone:2810435A13.Bcl2-like 2, full insert
 sequence.
 ACCESSION AK013244
 VERSION AK013244.1 GI:12850487
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (strain:C57BL/6J) 10, 11 days embryo cDNA to mRNA,
 clone:11b:RIKEN full-length enriched mouse cDNA library
 clone:2810435A13.

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

TITLE

High efficiency full-length cDNA cloning

JOURNAL

Meth. Enzymol. 303, 19-44 (1999)

MEDLINE

99279253

PUBMED

10349636

REFERENCE

2 (sites)

AUTHORS

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,

TITLE

Normalization and subtraction of cap-trapper-selected cDNAs to

JOURNAL

prepare full-length cDNA libraries for rapid discovery of new genes

MEDLINE

20499374

PUBMED

11042159

REFERENCE

3 (sites)

AUTHORS

Shibata,K., Itoh,M., Aizawa,K., Nagaoaka,S., Sasaki,N., Carninci,P.,

TITLE

Riken Integrated sequence analysis (RISA) system-384-format

JOURNAL

Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE

20530913

PUBMED

11076861

REFERENCE

4 (sites)

AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the

TITLE

Functional annotation of a full-length mouse cDNA collection

JOURNAL

Nature 409, 685-690 (2001)

MEDLINE

5 (bases 1 to 854)

PUBMED

11076861

REFERENCE

4 (sites)

AUTHORS

Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,

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Nature 409, 685-690 (2001)

MEDLINE

5 (bases 1 to 854)

PUBMED

11076861

REFERENCE

4 (sites)

AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the

TITLE

Functional annotation of a full-length mouse cDNA collection

JOURNAL

Nature 409, 685-690 (2001)

RESULT	9
AM258810	
LOCUS	
DEFINITION	540 bp mRNA linear EST 23-DEC-1999
ACCESSION	U074802.Y1 Sugano mouse kidney mKia Mus musculus cDNA clone
VERSION	IMAGE:2500506 5' similar to SW:BCLM_MOUSE P70345 ACOPIOSIS
KEYWORDS	REGULATOR BCL-W. [2] SW:BCLM_MOUSE ;, mRNA sequence.
SOURCE	AM258810.1 GI:6631791
ORGANISM	EST.
	house mouse.
	Mus musculus.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
	1 (bases 1 to 540)
	Marta, M., Hillier, L., Kueba, T., Martin, T., Beck, C., Wylie, T.,
	Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person
	E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
	Waterston, R. and Wilson, R.
TITLE	The WashU-NCI Mouse EST Project 1999
JOURNAL	Unpublished (1999)
COMMENT	Contact: Marta M/WashU-NCI Mouse EST Project 1999

FEATURES
 source
 1. .540
 Seq primer: custom primer used
 High quality sequence stop: 465.
 Location/Qualifiers

```

FEATURES
source
Location/Qualifiers
1..540
/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone_1 IMAGE:2300906"
/clone_1ib="Sugano mouse kidney mk1a"
/sex="female"
/dev_stage="adult"
/lab host="DH10B"
/note="Organ: kidney; Vector: pME18s-FL3; Site_1: DraIII
(CACCATGTCG); Site_2: DraIII (CACCATGTCG); 1st strand cDNA
was primed with an oligo(dT) primer
[AGTGGCGCTTTTGTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGGTGCGTCAACTGC], digested
and cloned into distinct DraIII sites of the pME18s-FL3
vector (5' site CACGCTGTCG, 3' site CACCATGTCG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTCTGCTCTAAAGCTGGG and 3' end
primer GCAGCTGACGCTGACACA."
BASE COUNT
98 a 165 c 170 g 107 t
ORIGIN
```

[illegible]

Db	232	CCGCTGCACCAAGCCATGCGGGGCTGCTGGAGAGACGAATTGTAACACCCGTTTCCGGCCAC	291
Qy	181	ttctctgcacgcgcgcgtcagctacacatgtaecccaagctcagccccaagacagctcacc	240
Db	292	TTCTCTGCACCGGGCGGTGAGCTACACGGTAGCCCCCGGCTCAGCCCAACACGGCTTAC	351
Qy	241	caagttcttcgcagcaacttcccaaggaggccctaacttggagcgcgtctgtggaattcttc	300
Db	352	CAGGTTTCCGACGACATTTTCCAAAGGGGGCCCTAACTGGGGCGCTTGTGTGGACATCTTT	411
Qy	301	gtctttggagctgcccctgctgtctgagatgttcaacaaagaatggacctttggtggga	360
Db	412	GTCATATGGGCTGCGCTGTGCTGAGAACTGTCAACAAAGAAATGTGACCTTTGGTGGGA	471
Qy	361	caaatgtcaagatgtgaatgctgctcaccctggagaaacgtctgcgcactgtgaatcccaagc	420
Db	472	CAATGTCATATGGAGATGGTGCGCTTACCTGTGGAGACACGCTCTGCTGACTGAT-CACAGC	530
Qy	421	atgtggagct 430	
Db	531	AGTGGGGGCT 540	

RESULT	10
LOCUS	B1910270
DEFINITION	B1910270 643 bp, mRNA linear EST 16-OCT-2001
ACCESSION	U030809.43F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5218294 5'
VERSION	B1910270
KEYWORDS	B1910270.1 GI:16173653
SOURCE	EST.
ORGANISM	human.
	Homo sapiens

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 643)	Mammalia; Eulacerta; Primates; Catarrhini; Hominiidae; Homo.	NIH-MGC http://mgc.nci.nih.gov/ .	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
	Contact: Robert Strausberg, Ph.D.	Email: cgabbs-remail.nih.gov		
	Tissue Procurement: Life Technologies, Inc.	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:	http://image.llnl.gov		
	Plate: L1AM11548	row: j	column: 23	
	High quality sequence start: 643.			

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location/Qualifiers
1. .643
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1ib="IMAGE:5218294"
/clone_1ib="NIH_MGC_118"
/tissue-type="leukocyte"
/lab_host="DH10B"
/note="vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."
BASE COUNT
129 a 184 c 216 g 114 t

```

Query Match	63.0%;	Score 366.8;	DB 10;	Length 643;
Best Local Similarity	86.8%;	Pred. No. 5e-80;		

Matches	415;	Conservative	0;	Mismatches	62;	Indels	1;	Gaps	1;
OY	1	atggcagccagccagcccaacccacacacagcgcctagctgagctttagtgcctat	60						
Db	140	ATGGCAGCCAGCCAGCTTCGCGCCACAGACAGCGGCTGTGAGTGCAGACTTGTAGGTTAT	199						
OY	61	agctcagcagagaaggatattgtctgtgagctgacctgtgggaagccacagccgcagac	120						
Db	200	AAGCTGAGGAGAGAGGATTATGTCTGTGAGAGCTGGCGCCCGGGGAGGCGCCAGACCTGCAC	259						
OY	121	ccgctgacccaagccacagcagcgtctgtgagacagatttgaaccgcgtttccgcgaac	180						
Db	260	CCGCTGACACCAAGCATTGCGGCGGACGCTGGAGATTCAGACCCGCTCCGCGGCACAC	319						
OY	181	tctctcagctgagcgcgtcagctacacgtgacccagcagctcagcccgcaagcgttcaac	240						
Db	320	TTCTCTGATCTGGCGGCTTCAGCTGACATGTGACCCAGGCTCAGCCACACACCTTCACAC	379						
OY	241	caggtttccgcagcagctttccacagggggccctcactgagggccgcttctgtgacattctt	300						
Db	380	CAGGCTCTCCGATGAACTTTTCAAGGGGGGCCCACTGGGGCGCGCTGTACCTCTCTT	439						
OY	301	gtcttggagcgtcgcctgtgtgtcgtgagagtgcacaaaga-aatgagcctttgtgtgtg	359						
Db	440	GTCTTTGGGGCGGACGCTGTGTGTGAGAGTGTACACAGAGAGCATGAAACCACTGGTGG	499						
OY	360	acaagtgcagagattgtagatgtgtgcctcctcgtgagacacgctcgtcgtcgtgacacag	419						
Db	500	ACAAGTGCAGGAGTGTGAGTGTGGCTTACTGTGAGACCGCGGCTGGCTGACTGATTCACAG	559						
OY	420	cagtgagcgtctgagcaggttcacagctctacagggagcgggacctgtgaggaagca	477						
Db	560	CAGTGGGGGCTGGAGCTGGAAGCTATCAAGCTCGAGTCAAGGAGATGAGAGAGAA	617						
RESULT	11	AA596919	362 bp	mrna	linear	EST	19-SEP-1997		
LOCUS	AA596919	VOZ1F08.r1 Barsstead mouse myotubes MRLB5 Mus musculus cDNA clone							
DEFINITION	IMAGE:1050567 5' similar to TR:EI23735 EI23735 R1 MRNA. ;, mrna								
ACCESSION	AA596919	GI:2412354							
VERSION	AA596919.1	GI:2412354							
KEYWORDS	EST.								
SOURCE	house mouse.								
ORGANISM	Mus musculus								
REFERENCE	1 (bases 1 to 362)								
AUTHORS	Marrin, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Scheinberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and								
TITLE	The WashU-HMI Mouse EST Project								
JOURNAL	Unpublished (1996)								
COMMENT	Contact: Mattia M/Mouse EST Project WashU-HMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:582143 Seq primer: -28m13 rev2 ET from Amersham High quality sequence stop: 334. Location/Qualifiers 1. 362 /organism="Mus musculus" /strain="C3H" /db_xref="taxon:10090"								

Query Match	55.9%;	Score	325.4;	DB	9;	Length	362;		
Best Local Similarity	98.2%;	Pred.	No. 6.6e-70;	<td></td> <td></td> <td></td>					
Matches	329;	Conservative	0;	Mismatches	6;	Indels	0;	Gaps	0;
OY	4	gacacccagcctcaacccacacacacagcgcctagtgagctttaggctatag	63						
Db	27	GGGACCCCAAGCCTCAACCCACAGACAGCGGCTGTGAGTGTGAGCTTGTAGGCTTAAAG	86						
OY	64	ctgaagcagaaggatattgtctgtgagctgagccctgggggaagggccagccgcgacccg	123						
Db	87	CTGAGGACAGAGGCTTATGTCTGTGAGCTGTGAGCTGCGCTGGGGAAGGCCACGCCGACCCG	146						
OY	124	ctgacacaaagcctatgagcgtctgtgagacagattttagagaccgctttccgcagccttc	183						
Db	147	CTGCACCAACCAATGCGTGTGCTGTGAGACGAGTTTGAGACCCGTTTCCGCCGACCTTC	206						
OY	184	tctgacctgagcgtcagctacacagctgacacagcgcctcagcccaagcagcttcaaccag	243						
Db	207	TCTGACTGGCGGCTGACGCTACACGTCGACCCAGGCTGACGCCACACAGCTTCAACCCAG	266						
OY	244	gttccagcagaactttccaaaggggccctcactaggggcgcgtctgtgacattcttctc	303						
Db	267	GTTCGCCAGCAACTTTTCCAAAGGGGGCCCTTAACCTGGGGCGGCTGTGTCATTTCTTGTTC	326						
OY	304	ttggggcgtccctgtgtgtgtgtagagatgtaacaa	338						
Db	327	TTTGGGCTGCCCTGTGTGTGAGAGTGTACAAA	361						
RESULT	12	BI764428	758 bp	mrna	linear	EST	25-SEP-2001		
LOCUS	BI764428	603050701F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5190792 5'							
DEFINITION	NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5190792 5'								
ACCESSION	BI764428	GI:15756006							

Plate: L1AM11477 row: a column: 01
High quality sequence stop: 753.
Location/Qualifiers

FEATURES

source

1..758
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="5190792"
/clone_id="NIH_MGC_116"
/lab_host="DH103"
/note="Organ: pooled colon, kidney, stomach; Vector: PCMV-Sport6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon, 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

BASE COUNT 140 a 216 c 228 g 174 t

Query Match 49.3% Score 286.8; DB 10; Length 758;
Best Local Similarity 90.5% Pred. No. 2.6e-60;
Matches 306; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

OY 1 atggcgacccagcgtctaacccagacacagcgtctagctgactttagcat 60
|||||
DB 139 ATGGCGACCCAGCCTGCGCCAGACACCGGCTCTGTGGCAGACTTTTGTAGTTAT 198
|||||
OY 61 aggttgagcagaaggttatgtctgtgagctggccctggggagagccagcgacgac 120
|||||
DB 199 AAGCTGAGCGAAGAGGTTATGTCTGTGAGCTGGCCCGGGAGAGGCCACACACTGAC 258
|||||
OY 121 ccgctgacacacagcattcgagctgtgagagcagattttagaccgcttccgcgcgac 180
|||||
DB 259 CCGCTGACCCAGCAGTGCAGGCGAGCTGGAGATGATTCGACCCGCTTCGGGCGCAC 318
|||||
OY 181 ttcttgacccgtcgctgacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgt 240
|||||
DB 319 TTCTCTGATCTGCGGCTCACTGCTGATGACCCCAAGCTCAGCCCAACGCTTCACC 378
|||||
OY 241 caggttccgagcgaactttccaaggggagccctaacctgagggcgctgtgacatctt 300
|||||
DB 379 CAGGTCTCGGATGAACCTTTTCAAGGGGGCCCACTGGGGCGGCTTGTAGCTCTTT 438
|||||
OY 301 gtcttggggcgctgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 338
|||||
DB 439 GTCTTTGGGGCTGCACTGTGTCTGAAGTGTTCCTCA 476
|||||

RESULT 13

BB856021

457 bp

mRNA

linear EST 26-NOV-2001

DEFINITION

BB856021 RIKEN full-length enriched, B16 F10Y cells Mus musculus
CDNA clone G370030007 5', mRNA sequence.

ACCESSION

BB856021

GI:17097475

VERSION

EST.

KEYWORDS

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

AUTHORS

1 (bases 1 to 457)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Akimura, T., Arakawa, K., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Kono, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T.

TITLE

JOURNAL

COMMENT

Watanabe, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
2001)
Unpublished (2001)
Contact: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura
, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multichannel sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nontandem cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

FEATURES

source

Location/Qualifiers
1..457
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="G370030007"
/clone_id="RIKEN full-length enriched, B16 F10Y cells"
/cell_type="B16 F10Y cells"
BASE COUNT 81 a 154 c 137 g 85 t

ORIGIN

Query Match 47.7% Score 277.4; DB 9; Length 457;
Best Local Similarity 98.7% Pred. No. 4.6e-58;
Matches 311; Conservative 0; Mismatches 1; Indels 3; Gaps 3;
OY 1 atggcgacccagcgtctaacccagacacagcgtctagctgactttagcat 60
|||||
DB 144 ATGGCGACCCAGCCTCAACCCAGACACAGGCTCTAGAGCTGTGATGCTAT 203
|||||
OY 61 aggttgagcagaaggttatgtctgtgagctggccctggggagagccagcgacgac 120
|||||
DB 204 AAGCTGAGCGAAGAGGTTATGTCTGTGAGCTGGCCCTGGGAGAGGCCACGCCGCGAC 263
|||||
OY 121 ccgctgacacacagcattcgagctgtgagagcagattttagaccgcttccgcgcgac 180
|||||
DB 264 CCGCTGACCCAGCAGTGCAGGCGAGCTGGAGACGATTGAGACCCGTTCCGCCGAC 323
|||||
OY 181 ttcttgacccgtcgctgacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgt 240
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DB 324 TTCTCTGATCTGCGGCTCACTGCTGATGACCCCAAGCTCAGCCCAACGCTTCACC 383
|||||
OY 241 caggttccgagcgaactttccaaggggagccctaacctgagggcgctgtgacatctt 300
|||||
DB 384 CAGGTCTCGGATGAACCTTTTCAAGGGGGCCCACTGGGGCGGCTTGTAGCTCTTT 440
|||||
OY 301 gtcttggggcgctgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 315
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DB 441 GTCTTTGGGGCTGCACTGTGTCTGAAGTGTTCCTCA 455
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RESULT 14
LOCUS B677345 749 bp mRNA linear EST 01-MAY-2001
DEFINITION 602624059P1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4748943 5',
mRNA sequence.
ACCESSION B677345
VERSION B677345
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 749)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM10601 row: f column: 16
High quality sequence stop: 732.
Location/Qualifiers
source
1. 749
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4748943"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-Sport6; Site-1: NotI;
Site-2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI-CGAP Library."
BASE COUNT 156 a 239 c 135 t
ORIGIN
Query Match 43.7%; Score 254.2; DB 10; Length 749;
Best Local Similarity 90.6%; Pred. No. 2.7e-52;
Matches 271; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 1 atggcagcccccagctcaaccacacagcagcctctagctgctgacttggagctat 60
DB 126 ATGGCGACCCCGAGCTCGGCCCGACACACAGGCGCTGTGGGACACTTGTAGTTAT 185
QY 61 agcttgagcagaaggtatgtctgtgagctgagcctggtgggaagccagccgagac 120
DB 186 AAGCTGAGGCGAGAGGGTTATGTCTGTGAGCTGGCCCGGGGAGGCGCCAGAGCTGAC 245
QY 121 ccgctgacacacacacatgagcgtgctgagacagattgagaccgcttccgcccagac 180
DB 246 CCGCTGACACCAAGCCATGCGGGGACGCTGGAGATGATTCAGACCCGCTTCGGCGCAC 305
QY 181 ttcttgacctgagcgtctacgtacacgtgaccccaaggtctcagcagcaagcttacc 240
DB 306 TTCTCTGATCTGGCGGCTCAGCTCATGTGACCCAGGCTTCAGCCCAACAGCTTCAC 365
QY 241 caggttccgagcaacttcccaagggggccctactgagggcgcttctgagcattctt 299
DB 366 CAGGCTCTCCAGTAACTTTTCAAGGGGGCCCAACTGAGGCGCGCTTGTAGCTTCTT 424

RESULT 15
LOCUS BF204905 601 bp mRNA linear EST 06-NOV-2000
DEFINITION 601866718P1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4106836 5',

ACCESSION BF204905
VERSION BF204905.1 GI:11098491
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 601)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLM987 row: d column: 05
High quality sequence stop: 561.
Location/Qualifiers
source
1. 601
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4106836"
/tissue_type="NIH_MGC_17"
/lab_host="DH10B (phage-resistant)"
/note="Organ: muscle; Vector: pORF6; Site-1: EcoRI;
Site-2: XhoI; cDNA made by oligo-dT priming.
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 110 a 176 c 201 g 114 t
ORIGIN
Query Match 42.4%; Score 246.8; DB 10; Length 601;
Best Local Similarity 81.7%; Pred. No. 1.7e-50;
Matches 358; Conservative 0; Mismatches 72; Indels 8; Gaps 6;
QY 9 cccagctcaaccag--acacagggctctagtgctgac-ttctgagctatagc 64
DB 164 CCCAGCTCGGCCCGACACACACCGGCTGTGGGACACATTTGTAGTTAAAGC 223
QY 65 tgaagcagaaggtatgtctgtgagctgagcctggggaagccagccgagccagc 124
DB 224 TGAGGCGAGAGGGTTATGTCTGTGAGCTGGCCCGGGAGGGGCCAGCAGCTGACCCAC 283
QY 125 tgcacacacatgagcgtctgagacagattgagacccgcttccgcccagccttc 183
DB 284 TGCACCAAGCAGCGCGGACGATGAGATGATGACACCGCTTCGCGCTCACCTTC 343
QY 184 tctgacctggcgtcactgct-acagctgaccccaaggtctgagccagcaagc-cttacc 241
DB 344 TGTGATCTGGCGGCTCAGCTCATGTATCCAGGCTCAAGCCCAACAGCACTTCACCC 403
QY 242 aggttcgagacac-ttcccaagggggccctactgagggcgcttctgagcattctt 300
DB 404 AGGCTCTCCGTAAGACTTTTGCAGAGGGGCCCAACTGGGGTTCCGTTGAGCTTCTTG 463
QY 301 gctcttggagctgcccctgctgtctgagagtgctaacaaagaatgagaccttggagg 360
DB 464 GTCTTGGGGCTGACACTGTCTGCTGAGAGTGTCAACAGAGATGAGACCACTGAGGGA 523
QY 361 caagtcagagatgtagtggtgagcctactgagacagctgctgagctgagatccacagc 420
DB 524 CAAATGAGAGAGTGAATGATGCTACTGTGAGACCGCGGTGTGCTATCTGATTCACAAAG 583

Thu Jun 6 16:39:26 2002

us-09-155-327e-8.rst

Page 12

QY	421	agtgcgcgtctggcggag	438
Db	584	AGAGTGGGGTGTGGGAG	601

Search completed: June 6, 2002, 11:24:34
Job time: 5590 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 6, 2002, 11:58:14 ; Search time 1853.13 Seconds
(without alignments)
6572.256 Million cell updates/sec

Title: US-09-155-327E-8
Perfect score: 582
Sequence: 1 atggcgagccaccagctcaac.....ccttttgcagcagatga 582

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_bhg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sy:*
12: gb_un:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_jmu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hhg_hum:*
31: em_hhg_inv:*
32: em_hhg_other:*
33: em_hhg_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description

1	578.8	99.5	582	10	MMU59746	US9746 Mus musculus
2	578.8	99.5	3476	10	AF030769	AF030769 Mus muscu
3	563.4	96.8	581	6	AX022531	AX022531 Sequence
4	563.4	96.8	581	6	AX030819	AX030819 Sequence
5	562.8	96.7	582	10	AF096291	AF096291 Rattus no
6	558.2	95.9	579	6	AR020779	AR020779 Sequence
7	524.4	90.1	582	9	HS059747	US9747 Human Bcl-w
8	521.2	89.6	3542	9	D87461	D87461 Human mRNA
9	519.6	89.3	583	6	AX022529	AX022529 Sequence
10	519.6	89.3	583	6	AX030817	AX030817 Sequence
11	519.6	89.3	1437	9	BC021198	BC021198 Homo sapi
12	515	88.5	579	6	AR020780	AR020780 Sequence
13	405.6	69.7	151212	2	AC079885	AC079885 Rattus no
14	405.6	69.7	181282	2	AC084240	AC084240 Rattus no
15	372.2	64.0	196292	2	CNS0000B	AL049829 Human chr
16	241.2	41.4	749	5	XR1	X82462 X.laavis R1
17	218.6	37.6	6049	5	AX345130	AX345130 Sequence
18	192.6	33.1	6049	6	AX345131	AX345131 Sequence
19	142.4	24.5	1252	4	AB073983	AB073983 Canis fam
20	140.8	24.2	702	4	AY005131	AY005131 Oryctolag
21	139.2	23.9	766	4	AF164517	AF164517 Ovis arie
22	137.6	23.6	541	4	AF245488	AF245488 Bos tauru
23	136	23.4	541	4	AF245487	AF245487 Bos tauru
24	136	23.4	541	4	AF245489	AF245489 Bos tauru
25	135	23.2	764	10	RN010579	U10579 Rattus norv
26	135	23.2	1742	6	BD006625	BD006625 A mutagen
27	135	23.2	1742	10	RN072350	U72350 Rattus norv
28	135	23.2	2232	10	RNCBLXLS	X82537 R.norvegicu
29	134.6	23.1	926	6	AR054021	AR054021 Sequence
30	134.6	23.1	926	6	AR118504	AR118504 Sequence
31	134.6	23.1	926	6	AR124952	AR124952 Sequence
32	134.6	23.1	926	6	AR144311	AR144311 Sequence
33	134.6	23.1	926	6	AR172594	AR172594 Sequence
34	134.6	23.1	926	6	E58777	E58777 Screening m
35	134.6	23.1	926	6	I52011	I52011 Sequence 5
36	134.6	23.1	926	9	HSBCLXL	223115 H.sapiens b
37	134.6	23.1	1236	9	AX085490	AX085490 Sequence
38	134.6	23.1	2575	9	BC019307	BC019307 Homo sapi
39	134.6	23.1	7372	6	E23357	E23357 Virus vecto
40	134.2	23.1	720	4	AF216205	AF216205 Sus scrof
41	134.2	23.1	752	4	SSJ001203	AJ001203 Sus scrof
42	133.4	22.9	1184	5	UGU26645	UGU26645 Gallus gall
43	131.2	22.4	1455	6	AX085496	AX085496 Sequence
44	130.2	22.4	726	10	RN034963	U34963 Rattus norv
45	130.2	22.4	726	10	S76513	S76513 bcl-x-apopt

ALIGNMENTS

RESULT 1
LOCUS MMU59746 582 bp mRNA linear ROD 29-SEP-1996
DEFINITION Mus musculus Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION U59746
VERSION U59746.1 GI:1572494

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 582)
Gibson, L., Holmgren, S.P., Huang, D.C., Bernard, O., Copeland, N.G.,
Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S.,
bcl-w, a novel member of the bcl-2 family, promotes cell survival
Oncogene 13 (4), 665-675 (1996)
96358615
2 (bases 1 to 582)
Gibson, L., Holmgren, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and
Cory, S.,
Direct Submission
Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and
Eliza Hall Institute of Medical Research, PO Royal Melbourne

FEATURES
 source
 Hospital, Parkville, Victoria 3050, Australia
 Location/Qualifiers
 1..582
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /chromosome="14"
 /cell_line="Baf3"
 1..582
 /gene="bcl-w"
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 /note="promotes cell survival; Bcl-2 homolog"
 /codon_start=1
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 /db_xref="GI:1572495"
 /translation="MNPASTPPTRALVADFGYKLRQKGYCGAGREGPADPLHO
 AMRAGDEFEFRFRRTSDLAOLHTPGSAQDFQVSDLEFGGPMGRVAFVFE
 GAALCAESVKNEMEPVGOVDMVALETRLADWHSSCGMAEFYALYGDGALLEAR
 RLREGNMAVRYTLTGAVLALVTGAFPAASK"
 BASE COUNT 107 a 158 c 200 g 117 t
 ORIGIN

Query Match 99.5%; Score 578.8; DB 10; Length 582;
 Best Local Similarity 99.7%; Pred. No. 6e-125;

Matches 580; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 atggagacccagcctcaacccagacacagggcctagtgcctgttagctat 60
 Db 1 ATGGAGACCCAGCCTCAACCCAGACACAGGGCTCTAGTGGCTGATGAGCTAT 60
 QY 61 aggcctgagcagaaggtatgtctgtgagctgcccctgggagagccagccgac 120
 Db 61 AAGCTGAGGAGGAGGCTTATGTCTGTGAGCTGGCCCTGGGAGAGCCAGCCGCGAC 120
 QY 121 ccgctgacacagcctgagcgtgctgagagagagtttagaccgttccgacgac 180
 Db 121 CCGCTGACACAGCCATGCGGGCTGCTGGAGACAGTTTGAACCCCTTTCGCCGAC 180
 QY 181 ttctctgacctgagcctcagctacagctgacccagcctcaacccagcagcttacc 240
 Db 181 TTCTCTGACCTGGCGCCCTCAGCTACAGTACCCAGCCCTCAGCCAGCAACCTTAC 240
 QY 241 caagttccagagactttcccaaggggcccctaactgagggccgtctgtgacattct 300
 Db 241 CAGGTTCCAGCAAACTTTTCCAAAGGGGCGCTTACCTGGGCGCTTGTGCACTTCTT 300
 QY 301 gtcttggagcctgcccctgtgtgctgagagagtgcaacaagaatgagccttgggga 360
 Db 301 GTCTTGGGGCTGCCCTGTGTGCTGAGAGAGTCTAACAAGAAATGAGCCCTTGTGGGA 360
 QY 361 caagtgacagattgatgagtgagcctcctgagagacagctgtgctgactgataccagc 420
 Db 361 CAAGTGACGAGATTGATGTGTGCTTACCTGAGACACAGTCTGCTGATCGATCCACAGC 420
 QY 421 agtggcgagcgtggcagagttcaagctctatacgggagacggggccctggagagagcagg 480
 Db 421 AGTGGGAGCTGGGGAGAGTTCAAGCTCTATATACGGGAGCGGGCCCTGGAGAGGACAGC 480
 QY 481 cgtctcggagagagcagcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 540
 Db 481 CGTCTCGGAGAGGAGAACTGGGCACTAGTGAGAGACAGTCTGACGGGGGCGCTGGGCACTG 540
 QY 541 ggggcccctgttaactgttagggcccttttctgtagcaagtga 582
 Db 541 GGGGCCCTGTAACTGTAGGGGCGCTTTTGTGCTAGCAAGTGA 582

RESULT 2
 LOCUS AF030769 3476 bp mRNA linear ROD 16-NOV-1997
 DEFINITION Mus musculus BCL-W (Bcl-w) mRNA, complete cds.

ACCESSION AF030769
 VERSION AF030769.1 GI:2623249
 KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 3476)
 Ross, A.J., Waymire, K.G., Moss, J.E., Parlow, A.F., Russell, L.D. and
 Macgregor, G.R.
 Bcl-w is required for testis homeostasis
 Unpublished
 2 (bases 1 to 3476)
 Ross, A.J. and Macgregor, G.R.
 Direct Submission
 Submitted (21-Oct-1997) Center for Molecular Medicine, Emory
 University, 1462 Clifton Road, Atlanta, GA 30322, USA
 Location/Qualifiers
 1..3476
 /organism="Mus musculus"
 /strain="C57BL/103"
 /db_xref="taxon:10090"
 /chromosome="14"
 /map="19.5 cm"
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 /gene="Bcl-w"
 1..82
 /gene="Bcl-w"
 /number=1
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 /number=2
 171..610
 /gene="Bcl-w"
 /number=3
 179..760
 /gene="Bcl-w"
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 /product="BCL-W"
 /protein_id="AAB86430.1"
 /db_xref="GI:2623250"
 /translation="MNPASTPPTRALVADFGYKLRQKGYCGAGREGPADPLHO
 AMRAGDEFEFRFRRTSDLAOLHTPGSAQDFQVSDLEFGGPMGRVAFVFE
 GAALCAESVKNEMEPVGOVDMVALETRLADWHSSCGMAEFYALYGDGALLEAR
 RLREGNMAVRYTLTGAVLALVTGAFPAASK"
 611..3476
 /gene="Bcl-w"
 /number=4
 3356..3364
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 /note="mRNA destabilization element"

polyA_signal
 BASE COUNT 796 a 814 c 991 g 875 t
 ORIGIN

Query Match 99.5%; Score 578.8; DB 10; Length 3476;
 Best Local Similarity 99.7%; Pred. No. 4.9e-125;

Matches 580; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 atggagacccagcctcaacccagacacagggcctagtgcctgttagctat 60
 Db 179 ATGGAGACCCAGCCTCAACCCAGACACAGGGCTCTAGTGGCTGATGAGCTAT 238
 QY 61 aggcctgagcagaaggtatgtctgtgagctgcccctgggagagccagccgac 120
 Db 239 AAGCTGAGGAGGAGGCTTATGTGTGAGCTGGCCCTGGGAGAGCCAGCCGCGAC 298
 QY 121 ccgctgacacagcctgagcgtgctgagagagagtttagaccgttccgacgac 180
 Db 299 CCGCTGACACAGCCATGCGGGCTGCTGGAGACAGATTGAGACCGCTTTCGCCGCGAC 358

QY	181	tctctyacctgacgctcaagctaacacgfygaccacagctctaacgcaacagcttacc	240
Db	359	TTCTCTACCTGGCGCTGACGTACACGTAACCCACAGCTCACGCCACGACGTTCTACCC	418
QY	241	caagttcccgacgaactttccaaaggggcccctaactyggccgtctctlygcatcttt	300
Db	419	CAGGTTTCCGACGAACTTTTCCAAAGGGGGCCCTTAACGTGGGGCGCTGTGGCATCTT	478
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Db	479	GTCCTTGGGGCGTCCCTGTGTGCTGACGAGTCAACAAACAAATGAGACCTTTGGTGGGA	538
QY	361	caagtgcaggaatgtagtgyggtgcttaacctgagaaacagctctgtgctactygtacatcaacagc	420
Db	539	CAAGTGCAGGATTTGGATGGTGGCTTACTCTTGGAGACAGCTTGCTGACTGTGATCCACAGC	598
QY	421	agtgcgagctbgygcgagattcacagcctctatacggggacgggcccctygaagsgacga	480
Db	559	AGTGGGGCTTGCGGGGAGTTCCACAGCTCTATACGGGGACGGGCCCTCGAGAGGACCG	658
QY	481	cgctbgyggaggggaaacttgagcatcaagtgaagacagttgctgcacgggggcccfyggcactg	540
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QY	541	ggggcccggtgaactgtaggggaccttttttctacgaagatga	582
Db	719	GGGGCCCTGCTGTAAGTGTAGGGGCCCTTTTCTTCTAGCAAGTGA	760

OY	121	ccgctgcaccaagaacccatgctcgagctgcctgcgaagacgaagtttgagaccocggtttccgcgcgaac	180
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Db	121	ccgctgcaccaagaacccatgctcgagctgcctgcgaagacgaagtttgagaccocggtttccgcgcgaac	180
OY	181	ttctctgaactgagcgtgaagctgaacagctgaaccacagagctcaacccagaacagctttacc	240
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Db	241	caagttccgcagcaactttccaaaggagccctaaactgagccgctctgtgacattctt	300
OY	301	gtctttgagagctgcctctgtgtgtcgtgaagatgttcaacaagaataatgtgaacgtttgtgtgga	360
Db	301	gtctttgagagctgcctctgtgtgtcgtgaagatgttcaacaagaataatgtgaacgtttgtgtgga	360
OY	361	caagtgcagaggtttgagatgctgacctactatgagacacgctctgctgtgaactgaccagc	420
Db	361	caagtgcagaggtttgagatgctgacctactatgagacacgctctgctgtgaactgaccagc	420
OY	421	atgtgcagctgagcgaattcacagctctatcacgaggagcggcctctgagagagcaagg	480
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OY	481	cgctcgcagagggaggaactggtacatcagttgagagcaagtgtcgaaggaggccgttggaactg	540
Db	481	cgctcgcagagggaggaactggtacatcagttgagagcaagtgtcgaaggaggccgttggaactg	540

RESULT	3	581 bp	DNA	linear	PAT 07-SEP-2000
AX022531	AX022531	Sequence 8 from Patent EP0932674.			
LOCUS	AX022531				
DEFINITION	Sequence 8 from Patent EP0932674.				
ACCESSION	AX022531				
VERSION	AX022531.1	GI:10046127			
KEYWORDS					
SOURCE	unidentified.				
REFERENCE	unclassified.				
AUTHORS	1 (bases 1 to 581)				
TITLE	Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.				
JOURNAL	A novel mammalian gene, bcl-1, belongs to the bcl-2 family of				
	apoptosis-controlling genes				
	Patent: EP 0932674-A 8 04-AUG-1999;				
	AMRAD OPERATIONS PTY LTD (AU)				
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BASE COUNT	105 a 164 c 195 g 117 t				
ORIGIN					
Query Match	96.8%;	Score 563.4;	DB 6;	Length 581;	
Best Local Similarity	98.1%;	Pred. No. 2.4e-121;			
Matches 570; Conservative	0;	Mismatches 11;	Indels 0;	Gaps 0;	

FEATURES	source	1.581	location/Qualifiers
REFERENCE		1 (bases 1 to 581)	
AUTHORS		Adams,V.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.	
TITLE		A novel mammalian gene, bcl-2, belongs to the bcl-2 family of apoptosis-controlling genes	
JOURNAL		Patent: WO 9735971-A 8 02-0CT-1997;	
		ADAMS JERRY MCKEE (AU) ; HOLMGREEN SHAUN P (AU) ; CORY SUZANNE (AU)	
		; GIBSON LEONTE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)	
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CDS			
		105 a	164 c 195 g 117 t
BASE COUNT			
ORIGIN			

Qy 1 atygagcaacccagcctcaaccccaagacacagggcctctagtggtctgttagagctat 60
Db 1 ATGCGACGCCACCGCTCAACCCCAACACACCGCTCTAGTGGCTGACTTTTAGGGTAT 60
Qy 61 aggcctagagcacaagaaggttatgtctgttgagctctgtgccttgggaagccagccgcgcgac 120
Db 61 AGGCTTAGGCGACGAAGGTTATGTCTGTGTGAGCTGTGGCTCTGGGGAAGGCCACGCCCGCGAC 120

Query Match	96.8%	Score 563.4;	DB 6;	Length 581;
Best Local Similarity	98.1%;	Pred. No. 2,4e-121;		
Matches 570;	Conservative	0;	Mismatches 11;	Indels 0;
Gaps 0;				
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Qy      121 ccgctgcacacaagcaltgcggctgctggaagacgaagatttgagaccgtttccgcgcac 180
Db      121 CCGCTGCACACAAGAGCTGGGCGCTCTGTGAGAGAGTTGAGACCCGTTTCCGCGGAC 180
Qy      181 ttctctgacctgagcgcccaagctacacgttgagcccaagctaacgcccagacgcttcaac 240
Db      181 TTCTCTGACCTGCGCGCTCAGCTACAGCTGACCCAGGCTCAGCCAGCAAGCGCTTCAAC 240
Qy      241 caagttccgagcaactttccaaaggagccctaactgagggccgtctgtgacattctt 300
Db      241 CAGGTTTCCAGAGACTTTTCCAAAGGGGCGCTTAAGTGGGCGCTGTGTGTGCTTTT 300
Qy      301 gtcttgaggctgctgctgtgtgtgagagtgcaacaagaatggagccttggtagga 360
Db      301 GCTTTGGGGCTGGCCCTGTGTGTGAGAGTGTCAACAAGAAATGAGACCTTTGTGGGA 360
Qy      361 caagtgcagattgagtggtgacctgagagacagctgctgctgagctgagctacagc 420
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Qy      421 agtgagcgctgagcgaggttcaacagctctatacagggagcgccctggagagcgagc 480
Db      421 AGTGAGCGCTGAGCGGAGCTTCAAGAGCTTATACGGGAGCGGCGCTGGAGAGACGACG 480
Qy      481 cgtctgcgagaggaactgagctcagtgagagacagctgctgagagggcgctggagcag 540
Db      481 CGTCTGCGAGAGGAGCACTGGGAGTGAAGTGAAGACAGTGGTGGAGCGGCGCTGGAGC 540
Qy      541 gggagcctggtgaactgtaggggaccttttgcctagcaagtg 581
Db      541 GGGGCGCTGGAAGTGAAGGCGCTTTTGTCTAGCAAGTG 581

RESULT 5
LOCUS   AF096291 582 bp mRNA linear ROD 28-FEB-2000
DEFINITION Rattus norvegicus Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION AF096291
VERSION   AF096291.1 GI:3747129
KEYWORDS
SOURCE   Norway rat.
ORGANISM Rattus norvegicus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
REFERENCE 1 (bases 1 to 582)
AUTHORS   Hamner,S., Skoglosa,Y. and Lindholm,D.
TITLE      Differential expression of bcl-w and bcl-x messenger RNA in the
           developing and adult rat nervous system
JOURNAL   Neuroscience 91 (2), 673-684 (1999)
MEDLINE   99292146
PUBMED    10366024
REFERENCE 2 (bases 1 to 582)
AUTHORS   Hamner,S., Skoglosa,Y. and Lindholm,D.
TITLE      Direct Submission
JOURNAL   Submitted (01-OCT-1998) Developmental Neuroscience, Uppsala
           University, Box 587, BMC, Uppsala 751 23, Sweden
FEATURES
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BASE COUNT  111 a 157 c 200 g 114 t

ORIGIN
Query Match      96.7%; Score 562.8; DB 10; Length 582;
Best Local Similarity 97.9%; Pred. No. 3,3e-121;
Matches 570; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy      121 ccgctgcacacaagcaltgcggctgctggaagacgaagatttgagaccgtttccgcgcac 180
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Qy      181 ttctctgacctgagcgcccaagctacacgttgagcccaagctaacgcccagacgcttcaac 240
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Qy      241 caagttccgagcaactttccaaaggagccctaactgagggccgtctgtgacattctt 300
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Qy      301 gtcttgaggctgctgctgtgtgtgagagtgcaacaagaatggagccttggtagga 360
Db      301 GCTTTGGGGCTGGCCCTGTGTGTGAGAGTGTCAACAAGAAATGAGACCTTTGTGGGA 360
Qy      361 caagtgcagattgagtggtgacctgagagacagctgctgctgagctgagctacagc 420
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Qy      421 agtgagcgctgagcgaggttcaacagctctatacagggagcgccctggagagcgagc 480
Db      421 AGTGAGCGCTGAGCGGAGCTTCAAGAGCTTATACGGGAGCGGCGCTGGAGAGACGACG 480
Qy      481 cgtctgcgagaggaactgagctcagtgagagacagctgctgagagggcgctggagcag 540
Db      481 CGTCTGCGAGAGGAGCACTGGGAGTGAAGTGAAGACAGTGGTGGAGCGGCGCTGGAGC 540
Qy      541 gggagcctggtgaactgtaggggaccttttgcctagcaagtg 582
Db      541 GGGGCGCTGGAAGTGAAGGCGCTTTTGTCTAGCAAGTG 582

RESULT 6
LOCUS   AR020779 579 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 1 from patent US 5789201.
ACCESSION AR020779
VERSION   AR020779.1 GI:3975394
KEYWORDS
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 579)
AUTHORS   Guastella,J.
TITLE      Genes coding for bcl-y a bcl-2 homologue

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Qy	181	ttctctcgaacctggcgcgtcaagctacacgtagccccaaaggttaagccccaaacggtctaac	240
Db	181	ttctctcgaacctggcgcgtcaagctacacgtagccccaaaggttaagccccaaacggtctaac	240
Qy	241	caggtttccgcgcgaaccttccaaaggggagccctaacttgggcgcgtcttcttgacattctt	300
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Qy	301	gtctttggggcgtgcctctgtgtcctagagatgttaacaaagaagaatgagccttttgttga	360
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Qy	361	caagctcagaatctgatatgttgcttaccttgagacacgctcttgctctactctgataccacagc	420
Db	361	caagctcagaatctgatatgttgcttaccttgagacacgctcttgctctactctgataccacagc	420
Qy	421	agtgagcgtctggcgagattcaacagctctatacgggagcgggacctgtgaagaaagcacaag	480
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Qy	582	ggggccctgttaactgttaagggccttttttcttaagcaagtga	582
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RESULT 10		DNA	linear	PAT 20-SEP-2000
AX030817				
LOCUS	AX030817	583 bp		
DEFINITION	Sequence 6 from Patent WO935971.			
ACCESSION	AX030817			
VERSION	AX030817.1	GI:10278311		

SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
source	unidentified.	1 (bases 1 to 583)	Adams,J.W., Holmgreen,S.P., Cory,S. and Gibson,L.M.	A novel mammalian gene, bcl-w, belongs to the bcl-2 family of apoptosis-controlling genes	Patent: WO 9735971-A 6 02-OCT-1997;	
	unclassified.		ADAMS JERRY MCKEE (AU) ; HOLMGREEN SHAUN P (AU) ; CORY SUZANNE (AU)			
			GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)			
				Location/Qualifiers		
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BASE COUNT      105 a    157 c    210 g    111 t
ORIGIN
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Db	1 ATGCGACCCCACTTCGGCCCCAAGACACGGGCTCTGTGTGGAAGACTTGAAGTTAT	60				
Oy	61 agctctgagcagaagatttatctctgtgaagtgcctctgggaaggccagccgcgaac	120				

Db	61	AAAGCTGAGGCGAAGGGTTATGTCGTGAGAGCTGGCCCCGGGGAGGGGCCAGACAGTCGAC	120
Qy	121	ccgctgcaccaacgaacacatgcgcgctgcgtgcgaacagatttgaagccgcttccgcgcgacc	180
Db	121	CCGCTGACACCAAGGCATGTCGGGGCAGCTGGAGATAGTTTCAGACCCGCTTCGGGGCACC	180
Qy	181	ttctctgaacctggcgcgcctcagctcacgtaaaccccaagctcgaaccgaacgcttcaac	240
Db	181	TTCTCTGATCTGGGGCTCAGCTGCATGTGACCCCAAGGCTCAGGCCAGCAACGCTTCACC	240
Qy	241	caagcttccgaacgaactttccaaagggggccctaacctggggcgcgtctgtggaattctt	300
Db	241	CAGGCTCGCAGACGAACCTTTTCAAGGGGGCCCCAACTGGGGCCGCTTGTAAGCCTTCTTT	300
Qy	301	gctcttggggcgtgcgcctgtgtgcgtgaagttgtcacaagaagaatgtgagccttgtgtga	360
Db	301	CTCTTTGGGGCTGCACCTGTGTGTGATGAGTGTCAACAAGAGATGTGAACCACTGGTGGA	360
Qy	361	caagtgcagaattgtgattgtgtgcctaacctgtgaaagaaagctctgcgtgacattgatacaacg	420
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Qy	421	atgtggcgtgtggcgcgaagttcacaagctataccggygaacggygcctcgtgaagagtgacgg	480
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Qy	481	cgctgcggaaggggaactcgggcataatgtgaagaagaagtgtcaacgggggcgctgacatg	540
Db	481	CGCTCGCGGAGGGGAACGTGGCATAGTGAAGACAGTGTCTAACGGGGCGGTGGCACATG	540
Qy	541	ggggccctgttaactgtlaagggccttcttgcctgaagtgaa	582
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RESULT	11				
LOCUS	BC021198	1437 bp	mRNA	linear	PRI 22-JAN-2002
DEFINITION	BC021198	Homo sapiens, BCL2-like 2, clone	MGC:10675	IMAGE:3944307,	mRNA,
ACCESSION	BC021198	complete cds.			
VERSION	BC021198.1	GI:18203706			
KEYWORDS	MGC.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
	1 (bases 1 to 1437)				
REFERENCE	Strausberg,R.				
AUTHORS	Direct Submission				
TITLE	submitted (14-JAN-2002)				
JOURNAL	National Institutes of Health, Mammalian				
	Cancer Genomics Office, National Cancer				
	Gene Collection (MGC).				

REMARK
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabp-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nihgri.nih.gov
Sherchenko, Y., Wetherby, R.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C.,
Dierlich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, O.L., Mastello, C., Mestrlian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantirpop, S., Thomas, P.J.,
Tiongson, E.E., Touchman, J.W., Tsurguen, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.


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KEYWORDS      HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE        Norway rat.
ORGANISM      Rattus norvegicus
AUTHORS       Eukaryota: Mammalia; Chordata: Craniata: Vertebrata: Euteleostomi:
              Muramalia; Eutheria; Rodentia: Sciurognathi; Muridae; Murinae;
              Rattus.
REFERENCE     1 (bases 1 to 151212)
              Beckstrom-Stenberg,S.M., Benjamin,B., Blakesley,R.W.,
              Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Gupta,J.,
              Ho,S.-L., Idol,J., Karlins,E., Lee-Lin,S.-Q., Legaspi,R., Lim,M.,
              Maduro,Q.L., Maduro,V.B., Mastrian,S.D., McCloskey,J.C.,
              McDowell,J., Pearson,R., Prasad,A., Snyder,B., Stantipop,S.,
              Thomas,J.W., Thomas,P.J., Tongson,E.E., Touchman,J.W.,
              Tsurgoun,C., Vogt,J.L., Walker/M.A., Wetherby,K.D. and Green,E.D.
              NISC Mouse Sequencing Initiative
TITLE         Unpublished
              2 (bases 1 to 151212)
              Green,E.D.
REFERENCE     Direct Submission
              Submitted (16-SEP-2000) NIH Intramural Sequencing Center, 8717
              Government Circle, Gaithersburg, MD 20877, USA
              On Nov 8, 2000 this sequence version replaced g1:10179358.
COMMENT       ----- Genome Center
              Center: NIH Intramural Sequencing Center
              Center code: NISC
              Web site: http://www.nisc.nih.gov
              Contact: nisc.mouse@nihri.nih.gov
              ----- Project Information
              Center project name: rk
              Center clone name: 246H18
              ----- Summary Statistics
              Sequencing vector: plasmid; n/a; 100% of reads
              Chemistry: dye-terminator Big Dye; 100% of bases
              Assembly program: Phrap; version 0.990319
              Consensus quality: 147800 bases at least Q40
              Consensus quality: 148726 bases at least Q30
              Consensus quality: 149333 bases at least Q20
              Insert size: 145000; agarose-fp
              Insert size: 150812; sum-of-contigs
              Quality coverage: 11.76x in Q20 bases; agarose-fp
              Quality coverage: 11.30x in Q20 bases; sum-of-contigs
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              * NOTE: This is a 'working draft' sequence. It currently
              * consists of 5 contigs. The true order of the pieces as
              * is not known and their order in this sequence record is
              * arbitrary. Gaps between the contigs are represented as
              * runs of N, but the exact sizes of the gaps are unknown.
              * This record will be updated with the finished sequence
              * as soon as it is available and the accession number will
              * be preserved.
              *
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              *          20441          20540: gap of unknown length
              *
              *          20541          41009: contig of 20469 bp in length
              *
              *          41010          41109: gap of unknown length
              *
              *          41110          65552: contig of 24443 bp in length
              *
              *          65553          65652: gap of unknown length
              *
              *          65653          110365: contig of 44713 bp in length
              *
              *          110366          110465: gap of unknown length
              *
              *          110466          151212: contig of 40747 bp in length.
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              vector_side:right"
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[illegible]

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Vogl, J.L., Walker, M.A., Wetherby, K.D. and Green, E.D.
NISC Mouse Sequencing Initiative
Unpublished
2 (bases 1 to 181282)
Green, E.D.
Direct Submission
Submitted (18-OCT-2000) NIH Intramural Sequencing Center, 8717
Givemont Circle, Galchertburg, MD 20877, USA
Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: <http://www.nisc.nih.gov>
Contact: nisc.mouse@nih.gov
Project Information
Center project name: r1
Center clone name: 103L21

----- Summary Statistics -----
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 179798 bases at least Q40
Consensus quality: 180132 bases at least Q30
Consensus quality: 180274 bases at least Q20
Insert size: 138000; agarose-fp
Insert size: 160000; pulse-field-gel
Quality coverage: 15.02x in Q20 bases; agarose-fp
Quality coverage: 12.95x in Q20 bases; pulse-field-gel
Quality coverage: 11.45x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 5430: contig of 5430 bp in length
* 5431 5530: gap of unknown length
* 5531 39503: contig of 33973 bp in length
* 39504 39603: gap of unknown length
* 39604 85792: contig of 46189 bp in length
* 85793 85892: gap of unknown length
* 85893 181282: contig of 95390 bp in length.
Location/Qualifiers
1. 181282

FEATURES

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/strain="Brown Norway"
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Best Local Similarity 86.6%; Pred. No. 8.6e-85;
Matches 447; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

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Db 49805 AGACATATGGGCTCTAATGATGTGAGCTGGCCCGGGAAGGCCCAACAGCAACCTGATTA 49864
OY 127 caccagacgatcgagctgctgagagagaggtttgagaccggtttccgagcacttctc 186
Db 49865 CACCAAGCATATGGGCTGTGAGACAAAGTATGAGACCCACTTCCAGACACCTTCTCT 49924
OY 187 gactgagcgtcactagctacagctgagccagctcagccagcagccttcacagctt 246
Db 49925 GACTGACCACTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 49984
OY 247 tccgagcaactttccaaaggggaggggaggggaggggaggggaggggaggggagggg 306
Db 49985 TCCAGCAACTTTTCCAAAGGGGGGCCCAACTAGGGCCATCTTGTGACATTTCTTTTCT 50044
OY 307 ggggctgacctgtgtgtcagagagtgtaacaaagaatgagccttggtagagcaagt 366
Db 50045 GGGGCTGCCCTGT 50104
OY 367 cagatgatgatgt 426
Db 50105 CAGGATGTGATGT 50164
OY 427 ggt 486
Db 50165 GGT 50224
OY 487 cggagggggaactgggagcagcagcagcagcagcagcagcagcagcagcagcagcag 546
Db 50225 AGGAGGGGAGGT 50284
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RESULT 15
CNS0000B 196292 bp DNA linear PRI 22-MAY-2001
LOCUS Human chromosome 14 DNA sequence BAC R-124D2 of library RPCL-11
DEFINITION from chromosome 14 of Homo sapiens (human), complete sequence.
ACCESSION AL049829
VERSION AL049829.4 GI:8217859
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 196292)
AUTHORS Heilig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P.,
Brottier, P., Catolico, L., Barde, V., Pelletier, E., Artiguenave, F.,
Levy, M., Eckenberg, R., Bruls, T., deBardirad, V., Crnaud, C.,
Gyapay, G., Saurin, W. and Weissenbach, J.
Sequencing of the human chromosome 14
Unpublished
2 (bases 1 to 196292)
Genoscope.
Direct Submission
Submitted (21-MAY-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
On Jun 3, 2000 this sequence version replaced gi:6138746.
----- Genome Center
Center: Genoscope / Centre National de Sequencage
Center code: GS
Web site: <http://www.genoscope.cns.fr/>
Contact: SeqRef@genoscope.cns.fr

The following BAC sequence is oriented from the T7 to the SP6 end.
Upstream BAC (overlapping the T7 end) : R-244E17
Downstream BAC (overlapping the SP6 end) : C-2201G16 (AC-AL132855)
----- Summary Statistics -----

Thu Jun 6 16:39:24 2002

us-09-155-327e-8.rge

Page 12

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 6, 2002, 10:38:27 ; Search time 66.15 Seconds
(without alignments)
2164.843 Million cell updates/sec

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Perfect score: 583
Sequence: 1 atggcgagccagcagctgcgc.....cttttgcctgcaagtga 583

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	572.6	98.2	579	2 US-08-978-523-2	Sequence 2, Appl
3	527.8	90.5	579	1 US-08-798-897-1	Sequence 1, Appl
4	527.8	90.5	579	2 US-08-978-523-1	Sequence 1, Appl
5	131	22.5	926	1 US-08-081-448-5	Sequence 5, Appl
6	131	22.5	926	2 US-08-470-670A-6	Sequence 6, Appl
7	131	22.5	926	3 US-08-481-739-1	Sequence 1, Appl
8	131	22.5	926	4 US-09-167-921-1	Sequence 1, Appl
9	131	22.5	926	4 US-09-277-020-39	Sequence 39, Appl
10	131	22.5	926	4 US-09-323-743-1	Sequence 1, Appl
11	131	22.5	926	4 US-08-461-511A-6	Sequence 6, Appl
12	131	22.5	926	5 PCT-US94-07089-6	Sequence 6, Appl
13	131	22.5	717	2 US-08-465-485A-20	Sequence 20, Appl
14	123.4	21.2	717	2 US-09-080-285-20	Sequence 20, Appl
15	123.4	21.2	4825	6 5459251-1	Patent No. 5459251
16	123.4	21.2	5086	2 US-08-465-485A-19	Sequence 19, Appl
17	123.4	21.2	5086	2 US-08-365-486A-14	Sequence 14, Appl
18	123.4	21.2	5086	3 US-09-080-285-19	Sequence 19, Appl
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20	123.4	21.2	5086	5 PCT-US93-05651-4	Sequence 4, Appl
21	123.4	21.2	5086	5 PCT-US93-06251-2	Sequence 2, Appl
22	123.4	21.2	5094	4 US-09-234-186-7	Sequence 7, Appl
23	123.4	21.2	5104	6 5506344-1	Patent No. 5506344
24	120.2	20.6	760	1 US-08-405-702A-11	Sequence 11, Appl
25	120.2	20.6	1846	4 US-08-365-486A-16	Sequence 16, Appl
26	120.2	20.6	1846	4 US-08-880-342-16	Sequence 16, Appl
27	119	20.4	615	2 US-08-465-485A-22	Sequence 22, Appl

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45	50.2	8.6	624	1 US-08-248-819A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-798-897-2
Sequence 2, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
Applicant: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSWEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET INFORMATION: 1483.0140001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-08-798-897-2

Query Match 98.2%; Score 572.6; DB 1; Length 579;
Best local similarity 99.3%; Pred. No. 1.8e-140;
Matches 575; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 atggcgagccagcagctgcgcagacacacagcagcagctgtgacacattttaggtat 60
DB 1 ATGGCGAGCCAGCAGCTGCGCCAGACACACAGCAGCAGCTGTGAGACATTGAGTTAT 60

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DB 301 GTCTTTGGGGGCTGACATGTCGTGAGAGTTCACAAAGAGATGGAACCACTGGTGGGA 360
QY 361 caagtgcaagagtgatagtgctcctacacgtgagacgagctgctgactgatacagac 420
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US-08-978-523-2
; Sequence 2, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540

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; INFORMATION FOR SEQ. ID NO.: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-08-978-523-2

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Query Match          98.2%; Score 572.6; DB 2; Length 579;
Best Local Similarity 99.3%; Pred. No. 1,8e-140;
Matches 575; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 1 atggcagcccaagcctcggcccaagacacagggcttggtagagactttagtattat 60
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DB 1 ATGGCAGCCCAAGCCTCGGCGCCCAAGACACAGGGGCTGTGTGGAACCTTGTAGGTTAT 60
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    |||
DB 121 CCACTGACCAACCAAGGCGGAGCTGAGATGAGATGAGAACCCGCTTCCGGCGAC 180
QY 181 ttctcgtatcggcgtcagctcagctgcatgtgaccccaagctcagccagcaagcttacc 240
    |||
DB 181 TTCTCTGATCTGGCGGCTGACGTGATGACCCCAAGCTTCAAGCCCAACAGCTTCAAC 240
QY 241 caagttccgacgaacttttcaagggggcccaacttgggcccgtttagcctctt 300
    |||
DB 241 CAGGTCCTCCAGTAGAATTTTCAAGGGGCGCCCAACTGGGCGCTTGTACTTCTTT 300
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    |||
DB 481 CGTCTGGGAGAGGGAACCTGGGCATCAGTGAAGACAGTGTGACGGGGCGGCGTGGCCTG 540
QY 541 ggggccctgtgtaactgttaggggctttttagtagcaag 579
    |||
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RESULT 3

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US-08-798-897-1
; Sequence 1, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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1  RESULT          5
2  US-08-081-448-5
3  : Sequence 5, Application US/08081448
4  : Patent No. 5646008
5  :
6  : GENERAL INFORMATION:
7  : APPLICANT: Thompson, Craig B.
8  : APPLICANT: Boise, Lawrence H.
9  : TITLE OF INVENTION: Vertebrate Apoptosis Gene:
10 : TITLE OF INVENTION: Compositions and Methods
11 : NUMBER OF SEQUENCES: 8
12 : CORRESPONDENCE ADDRESS:
13 : ADDRESSEE: Arnold, White & Durkee
14 : STREET: 321 No. 5646008th Clark Street, Suite 800
15 : CITY: Chicago
16 : STATE: IL
17 : COUNTRY: USA
18 : ZIP: 60610
19 :
20 : COMPUTER READABLE FORM:
21 : MEDIUM TYPE: Floppy disk
22 : COMPUTER: IBM PC compatible
23 : OPERATING SYSTEM: PC-DOS/MS-DOS
24 : SOFTWARE: PatentIn Release #1.0, Version #1.25
25 : CURRENT APPLICATION DATA:
26 : APPLICATION NUMBER: US/08/081,448
27 : FILING DATE: 19930622
28 :
29 : CLASSIFICATION: 424
30 :
31 : ATTORNEY/AGENT INFORMATION:
32 : NAME: No. 5646008thrup, Thomas E.
33 : REGISTRATION NUMBER: 33,268
34 : REFERENCE/DOCKET NUMBER: ARCD090
35 : TELECOMMUNICATION INFORMATION:
36 : TELEPHONE: 312-744-0090
37 : TELEFAX: 312-755-4489
38 :
39 : INFORMATION FOR SEQ ID NO: 5:
40 :
41 : SEQUENCE CHARACTERISTICS:
42 : LENGTH: 926 base pairs
43 : TYPE: nucleic acid
44 : STRANDEDNESS: single
45 : TOPOLOGY: linear
46 :
47 : MOLECULE TYPE: DNA (genomic)
48 : FEATURE:
49 :
50 : NAME/KEY: CDS
51 : LOCATION: 135..836
52 :
53 : US-08-081-448-5

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	Best Local Similarity	56.3%	Pred. No. 2.2e-25,		
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QY	158	tgaagaccgccttcggcgacactctctctgactctggcgcgctcaactcatgatacccaag	217		
Db	424	tttaactgtggatccggcgcgccgcatctcaatgacactgcagatcccaactccatatacccca	483		
QY	218	gctcagcccgcaagcgtctaccccaagcgtctccgcgcaactctttcaagggggccccaact	277		

Db	484	GGACGCGATATCAGACACTTTGAACAGGATGATGAACTCTTCCGGATGGGGTAAACT	54.3
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Query Match 22.5%; Score 131; DB 2; Length 926;
Best Local Similarity 56.3%; Pred. No. 2.2e-25;
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

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OY 98 ccggagagagagccagcagctgaccgcgtgcacacagccatgcgagcgtgagatgagt 157
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 364 cccggagagagtgatcccccattgacgaagaaagcagcgtgagagagcagcagcag 423
OY 158 tcgagagccgcctccgcgcacctctctgacatctgagcgtcagctgacatgacccca 217
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 424 ttgaaactgagcgtacccggcgacatttcaactgacatccacatccacatccacag 483
OY 218 gctcagccagcagacgcctccacccagctcgcagcgaactcttcaagggggcccaact 277
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 484 ggacacacatgacagacttttgaaacagtagaagaaacttccggagatgggtaaaact 543
OY 278 ggggcccgccttgagcctctcttcttcttgggagctgacatgtgtgctgagagtgta 337
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 544 gggggtgacattggtggttttcttcttcttcttcttcttcttcttcttcttcttct 603
OY 338 agagagatgagacacactggtgagcagagtgagagtgagtgagtgagtgagtgagcgc 397
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 604 agcagagatgacagtagtattgtagtgcgacatgcacgttgatggccattacatgacac 663
OY 398 ggcgtgctgactgagatccacagcagtgaggggctgagcgtgagtgagtgagtgag 457
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 664 acctagagccttgatgacgaagaaagcggcgatgacatttgggaactctgagagga 723
OY 458 acggagccctgagagggcgcgctcgtcgtgagggagagagagagagagagagagag 517
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 724 acaatgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 783
OY 518 tgcgtacggggggcg 532
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 784 gcattgactgtggccg 798
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RESULT 7
US-08-481-739-1
Sequence 1, Application US/08481739
Patent No. 6143291

GENERAL INFORMATION:
APPLICANT: June, Carl H. and Thompson, Craig B.
TITLE OF INVENTION: METHODS FOR ENHANCING T CELL SURVIVAL
TITLE OF INVENTION: BY AUGMENTING BCL-XL PROTEIN LEVELS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESS: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,739
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION NUMBER: US 08/435,518
FILING DATE: 04-MAY-1995

ATTORNEY/AGENT INFORMATION:
NAME: Deconth, Giulio A. (GAD)
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: RPI-034CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 135..836
US-08-481-739-1

Query Match 22.5%; Score 131; DB 3; Length 926;
Best Local Similarity 56.3%; Pred. No. 2.2e-25;
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

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OY 98 ccggagagagagccagcagctgaccgcgtgcacacagccatgcgagcgtgagatgagt 157
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 364 cccggagagagtgatcccccattgacgaagaaagcagcgtgagagagcagcagcag 423
OY 158 tcgagagccgcctccgcgcacctctctgacatctgagcgtcagctgacatgacccca 217
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DB 424 ttgaaactgagcgtacccggcgacatttcaactgacatccacatccacatccacag 483
OY 218 gctcagccagcagacgcctccacccagctcgcagcgaactcttcaagggggcccaact 277
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DB 484 ggacacacatgacagacttttgaaacagtagaagaaacttccggagatgggtaaaact 543
OY 278 ggggcccgccttgagcctctcttcttcttgggagctgacatgtgtgctgagagtgta 337
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 544 gggggtgacattggtggttttcttcttcttcttcttcttcttcttcttcttcttct 603
OY 338 agagagatgagacacactggtgagcagagtgagagtgagtgagtgagtgagtgagcgc 397
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DB 604 agcagagatgacagtagtattgtagtgcgacatgcacgttgatggccattacatgacac 663
OY 398 ggcgtgctgactgagatccacagcagtgaggggctgagcgtgagtgagtgagtgag 457
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 664 acctagagccttgatgacgaagaaagcggcgatgacatttgggaactctgagagga 723
OY 458 acggagccctgagagggcgcgctcgtcgtgagggagagagagagagagagagagagag 517
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 724 acaatgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 783
OY 518 tgcgtacggggggcg 532
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DB 784 gcattgactgtggccg 798
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RESULT 8
US-09-167-921-1
Sequence 1, Application US/09167921A
Patent No. 6172216

GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett P.
APPLICANT: Nickoloff, Brian J.
APPLICANT: Zhang, Qingqing
TITLE OF INVENTION: Adipose Modulation of bcl-x Expression
FILE REFERENCE: ISPH-0324
CURRENT APPLICATION NUMBER: US/09/167,921A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1
LENGTH: 926
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (135)..(836)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: L20121 Genbank

; DATABASE ENTRY DATE: 1994-07-26
 US-09-167-921-1

Query Match	22.5%	Score 131;	DB 4;	Length 926;
Best Local Similarity	56.3%;	Pred. No. 2.2e-25;		
Matches 245;	Conservative 0;	Mismatches 190;	Indels 0;	Cons 0

[illegible]

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RESULT 9
US-09-277-020-39
; Sequence 39, Application US/09277020
; Patent No. 6210892
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
; FILE REFERENCE: ISPH-0339
; CURRENT APPLICATION NUMBER: US/09/277, 020
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 09/167, 921
; EARLIER FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-277-020-39

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[illegible]

Db	424	ttagactgvcggtacccggcgcggtacatcagttgacattcccaagctccacatccacaccccaag	4833
QY	218	gctcaagcccaagaaacgctctccaccacagctgcctccgaagaaactcttccaaaggggcccccaact	2777
Db	484	ggacacatcatcagagcgtttgaaacacggtgaaatgaaatccttcccggaatgaggtaaact	5433
QY	278	ggggccgcgcctcttgacgctctcttgcctcttgggcgtccacatgtgctgcagagtgatccaca	3377
Db	544	ggggtctgcacatttgcgctcttctctccctccgcgggcacacgttgcgtggaagcgatgaca	6033
QY	338	aggagaatgnaaaccaatctggctgggaacaagtcgaagcgatgagatgagtcgactcaactctggaagcgc	3937
Db	604	aggagaatgcaggtatctggctggaagtcgaaatcgacagactctggatctgcacattcaactgaatgacc	6633
QY	398	ggctgctgctgactgtgattccacacagcagctgggcgctggcgcgaggttccacagcgtctatacgggg	4573
Db	664	acctagagccttgatggatcccaagagaagaacggcgctggtgataccttcttgagaaactctaaaggaa	7233
QY	456	aacgggggcccttgagagagacgcgcgcctctgcgcggagaggaagaaacttggtacatcagtgaaagaca	5173
Db	724	acaatgcagcagcagcagagcgccgaagaagcgacagaaacgcttcaaacgcgtgttccctgaacgg	7833
QY	518	tgctgacggggggccg	532
Db	784	gcattgactctgvcggtg	798

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US-09-323-743-1
: Sequence 1, Application US/09323743
: Patent No. 6214986
: GENERAL INFORMATION:
: APPLICANT: Bennett, C. Frank
: APPLICANT: Dean, Nicholas M.
: APPLICANT: Montia, Brett P.
: APPLICANT: Nickoloff, Brian J.
: APPLICANT: Zhang, Qinqing
: TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
: FILE REFERENCE: ISFH-0368
: CURRENT APPLICATION NUMBER: US/09/323,743
: EARLIER FILING DATE: 1999-06-01
: EARLIER APPLICATION NUMBER: 09/277,020
: EARLIER FILING DATE: 1998-03-26
: EARLIER APPLICATION NUMBER: 09/167,921
: EARLIER FILING DATE: 1998-10-07
: NUMBER OF SEQ ID NOS: 66
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 926
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (135)..(836)
: PUBLICATION INFORMATION:
: DATABASE ACCESSION NUMBER: L20121 Genbank
: DATABASE ENTRY DATE: 1994-07-26
US-09-323-743-1

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	Query Match	22.5%	Score 131;	DB 4;	Length 926;
	Best Local Similarity	56.38;	Pred. No. 2.2e-25;		
	Matches 245;	Conservative	0;	Mismatches 190;	Indels 0; Gaps 0;
OY	98	cctggagagcgccacgacgtcgaaccgccttcacacaagccaatgcggacagctcggaatgagt	157		
Dd	364	cccggaggatcgatcccccatcagtgcaagctaagaacaagccgcgaaggagcgagcaagcagat	423		
OY	158	tctggagaccgccttcctcgcgaccaattctcttgcatactltygcgycacacatcagltgtaaccaa	217		
Dd	424	ttgaactcgcgtgatccgcgcgcgcatctcagatlgacttgacatccccagctccatcataccccca	483		
OY	218	gctcagcccaagcaaacgtctcacccagctcctccagacgaactttttcaagggggcccaact	277		

[illegible]

MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 135..836
 PCT-US94-07089-6

Query Match 22.5% Score 131; DB 5; Length 926;
 Best Local Similarity 56.38; Pred. No. 2.2e-25;
 Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

98 ccgggaggggcccagctgaccgctgcccacagacatgcccagggagatgagt 157
 Db CCCGGGAGGTGATCCCATGCGACAGATGAAGCAAGCGCTGAGGAGCGAGCGAGT 423
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 Db TTGAACCTGGGTACCGGGGAGATTCAGTACCTGACATCCAGCTCCACATCACCAG 483
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 Db GGAGAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACCTTCCGGATGGGTAACCT 543
 278 gggcgccctgtgagcttcttcttcttcttcttcttcttcttcttcttcttct 337
 Db GGGGTCCATTGTGGCTTTTCTCTCTCGCGGGGCGGCTGCGTGAAGCGTAGACA 603
 338 aggaagatgaaacacactgtgagcaagtgcaagagtggtgctgctacccggaagcg 397
 Db AGGAGATGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 663
 398 ggcctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 457
 Db ACCTAAGCTTGTGATTCAGAGAAAGGCGGCTGGGATCTTTGTGAACTATAGGA 723
 458 acggggccctgagagggcgcgctctcgcggagaggaactgggcatcagatgagagac 517
 Db ACATATCAGACAGCGGAGAGCGAAGGCGCAAGAACGCTTCAACCGCTGTTCTGTGACG 783
 518 tcctgacggggggcg 532
 Db GCATGACTGTGGCGG 798

RESULT 13

US-08-465-485A-20
 Sequence 20, Application US/08465485A
 Patent No. 5831066
 GENERAL INFORMATION:
 APPLICANT: Reed, John
 TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
 ADDRESS: P.C.
 STREET: 1755 S. Jefferson Davis Hwy., Suite 400
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/465,485A
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/124,256
 FILING DATE: 20-SEP-1993
 PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 07/840,716
 FILING DATE: 21-FEB-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/288,692
 FILING DATE: 22-DEC-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Fortney, Andrew D.
 REGISTRATION NUMBER: 34,600
 TELEPHONE: (408) 436-2070
 TELEPHONE: (408) 436-2075
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 717 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..717
 US-08-465-485A-20

Query Match 21.2% Score 123.4; DB 2; Length 717;
 Best Local Similarity 58.6%; Pred. No. 1.9e-23;
 Matches 214; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

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 Db GCGGGGCTCGCGCTGACCGCGGCTGCACACTGTGATGATGATGATGATGATGATGAT 303
 151 gatgagctcgaagccgctccgctcgcgcactctctctgctgagcgctcagctgcatgtg 210
 Db GACGACTTCTCCCGCGCTACCGCGCGGCTGCGGAGATGTCACGACGATGTCACCTG 363
 211 acccagcgtcagccagcaagcttcaaccaggtctcgcagcgaactttcaaggggcg 270
 Db ACCGCTTACCGCGCGGCGGCTTTCACAGGCTGATGATGATGATGATGATGATGATGAT 423
 271 cccaactgagggcgctgtgagcttcttcttcttcttcttcttcttcttcttcttct 330
 Db GTGAAGTGGGAGAGATTTGCTTCTTGAAGTTCGTTGGGCTGATGATGATGATGATGATGAT 483
 331 gtcaacaaaggagatggaacacactgtggaacagtgcagagtgatgtgtggtacgtg 390
 Db GTCAACCGGAGATGTCGCCCTGTGTGACAAATGCGCCCTGTGATGATGATGATGATGATGAT 543
 391 gagaacgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 450
 Db AACCGGACCTGACACCTGATTCAGATACGAGGCTGGGATGCTTGTGGAAGTGTG 603
 451 taagg 455
 Db TACGG 608

RESULT 14

US-09-080-285-20
 Sequence 20, Application US/09080285
 Patent No. 6040181
 GENERAL INFORMATION:
 APPLICANT: Reed, John
 TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
 ADDRESS: P.C.
 STREET: 1755 S. Jefferson Davis Hwy., Suite 400
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.

Thu Jun 6 16:39:18 2002

us-09-155-327e-6.rni

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 6, 2002, 09:51:24 ; Search time 2348.74 Seconds
(without alignments)
3350.190 Million cell updates/sec

Title: US-09-155-327E-6
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Scoring table: IDENTITY_NUC
Gapex 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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2: em.esthum:*
3: em.estin:*
4: em.estnu:*
5: em.estov:*
6: em.estpl:*
7: em.estro:*
8: em.htc:*
9: gb.est1:*
10: gb.est2:*
11: gb.htc:*
12: gb.gss:*
13: em.gss_hum:*
14: em.gss_inv:*
15: em.gss_pln:*
16: em.gss_vtl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	488.2	83.7	697	10	BI770566 603060362
6	422.4	72.5	643	10	BI910270 603060493
7	400.2	68.6	815	10	BF785386 602111728
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11	328.4	56.3	758	10	BI764428 603050701
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15	257.6	44.2	433	9	AA326901 20104 MAR
16	241.6	41.4	457	9	BB856021 BB856021
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21	160.6	27.5	416	9	AM159063
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24	148.8	25.5	549	12	AQ665088
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26	139.2	23.9	648	9	AL632408
27	135.6	23.3	455	12	AC0401160
28	133.6	22.9	862	10	BG973530
29	132.8	22.8	913	10	BG244406
30	129.8	22.3	687	10	BE293685
31	129.4	22.2	700	10	BG831301
32	127.6	21.9	697	10	BI457116
33	127.6	21.9	965	10	BM457276
34	127.4	21.9	699	10	BE870269
35	126.4	21.7	974	10	BE250036
36	126.2	21.6	513	10	BM363392
37	125.8	21.6	404	9	AT716839
38	123.2	21.1	818	10	BG824757
39	123.2	21.1	890	9	AL537680
40	122.2	21.0	642	9	BI163814
41	122.2	20.9	690	10	BT060637
42	121.8	20.9	1035	10	BI409987
43	121.6	20.9	836	10	BM018295
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45	121.4	20.8	808	10	BI222971

ALIGNMENTS

RESULT 1
LOCUS AL157542 804 bp mRNA linear EST 24-FEB-2000
DEFINITION DKFZP761D0816.t1 761 (synonym: hamy2) Homo sapiens cDNA clone
AL157542
VERSION AL157542.1 GI:7057943
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS Ansoorge,W., Winkner,U., Mewes,W., Well,B. and Wiemann,S.
TITLE EST (Ansoorge,W., Winkner,U., Mewes,H.W., Well,B. and Wiemann,S.)
JOURNAL Unpublished (1999)
COMMENT Contact: Ansoorge W

MIPS
Am Klopferstr. 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKFZP761D0816) is available at the RZPD in Berlin.
Please contact the RZPD, Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1. 804
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZP761D0816"
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/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI"

BASE COUNT
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ORIGIN

Query Match 95.2%; Score 554.8; DB 9; Length 804;
 Best Local Similarity 99.1%; Pred. No. 6.3e-116;
 Matches 578; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 1 atggagaccacagcctcggccacagacacagagcctgtgtgacagcttgaattat 60
 Db 134 ATGGAGACCCAGCCTCGGCCAGACACAGGGCTGTGTGACAGCTTGTAT 193
 QY 61 aagctgaagcgaaggggtatgtctgtgagcttgcccgaggagggccagagctgac 120
 Db 194 AAGCTGAGGCGAAGGGGTATGTCTGTGAGCTGGCCCGGGAGGGCCAGAGCTGAC 253
 QY 121 ccgctgacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
 Db 254 CCGCTGACACAGCCATGCGGCGAGCTGGAGATGATTCAGACCCGCTTCCGGCCAC 313
 QY 181 ttctctgactgtgctcagctgacatgtgacccacagcagcagcagcagcagcagc 240
 Db 314 TTCTCTATCTGGCGGCTGACGTGACATGTGACCCAGGCTCAGCCACAGCTTCACC 373
 QY 241 caagtcacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300
 Db 374 CAGGTCTCGATGACTTTTCAAGGGGGCCCACTGGGCGCTTGTACCTTCTTT 433
 QY 301 gctcttgaggctcagctgtgtgtgagagtgacaaagagatgaaacagctgtgga 360
 Db 434 GTCTTGGGGCTGCTGCTGTGTGAGAGTGTCAACAAAGAGATGAACACTGTGTGGA 493
 QY 361 caagtcagagagtgatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 420
 Db 494 CAAGTCAGAGAGT 553
 QY 421 aagtgaggctgtgag 480
 Db 554 AGTGGGGGCTGGCGGAGTTCAACACTCTATACGGGGGAC -GGGCGCTGAGAGAGCGGG 612
 QY 481 cgtctcggag 540
 Db 613 CGTCTGGGAGAGGAGACAGTGCATCACTGAGAGACAGTGTGACGGGGCGTGGCACT - 671
 QY 541 ggggcccgtgtactgtgagggcctttttgttagcaagtgaa 583
 Db 672 GGGGCGCTGCTAACTGTAGGGGCGCTTTTGTCTAGCAAGTGAA 714

RESULT 2
 BE793530 1030 bp mRNA linear EST 20-SBP-2000
 LOCUS BE793530 1030 bp mRNA linear EST 20-SBP-2000
 DEFINITION 601590016F1 NIH_MGC_7 Homo sapiens CDNA clone IMAGE:3944307 5',
 mRNA sequence.
 ACCESSION BE793530
 VERSION BE793530.1 GI:10214832
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 1030)
 NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: DCTD/DRP
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
 Plate: LNC600 row: p column: 04

FEATURES
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 High quality sequence stop: 709.
 Location/Qualifiers
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 /note="Organ: lung; Vector: pOTB7; Site: 1; XhoI: Site_2;
 EcoRI: cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 190 a 284 c 386 g 170 t
 ORIGIN

Query Match 94.9%; Score 553.2; DB 10; Length 1030;
 Best Local Similarity 96.9%; Pred. No. 1.6e-115;
 Matches 564; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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 Db 144 ATGGAGACCCAGCCTCGGCCAGACACAGGGCTGTGTGACAGCTTGTAT 203
 QY 61 aagctgaagcgaaggggtatgtctgtgagcttgcccgaggagggccagagctgac 120
 Db 204 AAGCTGAGGCGAAGGGGTATGTCTGTGAGCTGGCCCGGGAGGGCCAGAGCTGAC 263
 QY 121 ccgctgacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
 Db 264 CCACTGACCAAGCCATGCGGCGAGCTGAGATGATTCAGACCCGCTTCCGGCGACC 323
 QY 181 ttctctgactgtgctcagctgacatgtgacccacagcagcagcagcagcagcagc 240
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 QY 241 caggtctcggag 300
 Db 384 CAGGTCTCGATGACTTTTCAAGGGGGCCCAACTGGGGCGCTTGTAGCTTCTTT 443
 QY 301 gctcttgaggctcagctgtgtgtgagagtgacaaagagatgaaacagctgtgga 360
 Db 444 GTCTTGGGGCTGCACTGTGTGAGAGTGTCAACAAAGAGATGAACTGTGGA 503
 QY 361 caagtcagagagtgatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 420
 Db 504 CAAGTCAGAGAGT 563
 QY 421 agtgaggctgtgag 480
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 QY 481 cgtctcggag 540
 Db 624 CGTCTGGGAGAGGAGAGCTGCATCACTGAGAGACAGTGTCTGACGGGGCGTGGCACTG 683
 QY 541 ggggcccgtgtactgtgagggcctttttgttagcaagtgaa 582
 Db 684 GGGGCGCTGCTAACTGTAGGGGCGCTTTTGTCTAGCAAGTGAA 725

RESULT 3
 AK015644 1949 bp mRNA linear HTC 19-JAN-2002
 LOCUS AK015644 1949 bp mRNA linear HTC 19-JAN-2002
 DEFINITION Mus musculus adult male testis cDNA, RIKEN full-length enriched
 library, clone:493048BD08:Bcl2-like 2, full insert sequence.

	TITLE	JOURNAL	PUBLISHED	REFERENCE	AUTHORS
OY	481	C9CTCGGGGAGGAGGAACTGGATGCATGAATGAGGAGCAAGTGTCTGACGAGGAGCCGTCgactg	540		
Db	612	C9CTCGCGGAGGAGGAACTGGGATGCATGAATGAGGAGCAAGTGTCTGACGAGGAGCCGTCgactg	671		
OY	541	ggggccctgtgaactgttaggggccttttcttgtagcaagtga	582		
Db	672	GGGGCCTCGTAACGTAGTGAGGCCCTTTTCTTGCTAGACAAGTTGA	713		
RESULT	4				
LOCUS	AK004680				
DEFINITION	Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:11200009L24:Bcl2-like 2, full insert sequence.				
ACCESSION	AK004680				
VERSION	AK004680.1				
KEYWORDS	HNC; CAP trapper.				
SOURCE	Mus musculus (strain:C57BL/6J) adult male lung cDNA to mRNA, clone:11200009L24.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Mus.				
AUTHORS	Carninci,P. and Hayashizaki,Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2 (sites)				
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20493374				
PUBMED	11042159				
REFERENCE	3 (sites)				
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Komoto,H., Akiyama,U., Nishi,K., Kitsuana,T., Tashiro,H., Itoh,M., Suni,N., Ishii,T., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsunoto,H., Sakaguchi,S., Ikegami,T., Kasaiwaiki,K., Fujiwaka,S., Inoue,K., Ozawa,Y., Izawa,M., Ohara,E., Matshiki,M., Yonekura,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system -384 format sequencing pipeline with 384 multicapillary sequencer				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
MEDLINE	20350913				
PUBMED	11076861				
REFERENCE	4 (sites)				
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.				
TITLE	Functional annotation of a full-length mouse cDNA collection				
JOURNAL	Nature 409, 685-690 (2001)				
MEDLINE	5 (bases 1 to 3487)				
PUBMED					
REFERENCE					
AUTHORS	Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bull,C., Carinici,P., Fukuda,S., Fukushima,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hirooka,T., Horii,F., Humo,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawaji,J., Koijima,Y., Komoto,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Schirral,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sobue,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamana,K.I., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.				
TITLE	Direct Submission				
JOURNAL	Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome				

COMMENT	FEATURES	source
Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute: 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)		
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.		
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAGGCGCCGCACTCGAGCTGTTTCTTTTCTTNN 3'], cDNA was prepared by using Trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence 15' GAGAGAGAGAGACTCAAGAGCTCAATTTATTTATTAACCCCTCCCTCC 3'. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOLR.		
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Best Local Similarity 94.2%; Pred. No. 1.4e-109;		
Matches 548; Conservative 0; Mismatches 34; Indels 0; Gaps 0;		
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209 ATGGCAGCCCGCAGCCTCAACCCCAACACACAGGCGCTACTGTGCTACTTTTAAAGCTAT 268		
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269 AACCTGAGCGAGAGGGTATGTCTGTGTGAGACTGCGCCCTGGGGAAGCCGACCCGAC 328		
121 cgccttcaccacaagcatctgaggagcttgcagatgagttcgagaccgccttcgcggcacc 180		
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|||||
Db 449 CAGGTTTCGACGACACTTTTCCAAAGGGGGCCCAACTGGGGCGCTTGTGCAATCTTT 508
Oy 301 gtcttgaggctgacactgtgtctgagagtgtaacaagaagatggaaccactgtgtgga 360
Db 509 GTCTTTGGGGGTGCGCTGTGCTGAGAGTGTCAACAAAGAAATGAGGCTTTGGGGGA 568
Oy 361 caagtgcagaagatgagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 420
Db 569 CAAGTGCAGAGTGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 628
Oy 421 agtggagctgagcagatcacagctctatacagggagcgggacctgtgagagagcgag 480
Db 629 AGTGGGGCTGTGGGGAGTTCACAGCTCTATACGGGAGCGGGCCCTGTGAGAGGACGG 688
Oy 481 cgtctcgaggaggaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 540
Db 689 CGTCTGCGGAGGGGACATGGGCAATGATGAGAGAGTGTGTGTGTGTGTGTGTGTGT 748
Oy 541 gggggccctgtaactgtaggggaccttttctgttagcaagtga 582
Db 749 GGGGCCCTGTGATCTGTAGGGGCGCTTTTGTCTAGCAAGTGA 790

RESULT 5 697 bp mRNA linear EST 25-SEP-2001
LOCUS B1770566 603060362r1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5209862 5'
DEFINITION mRNA sequence.
ACCESSION B1770566
VERSION B1770566.1 GI:15762144
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 697)
NIH-MGC http://mhc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM1526 row: k column: 15
High quality sequence start: 21
High quality sequence stop: 695.
Location/Qualifiers
1. 697
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5209862"
/clone_id="NIH_MGC_122"
/lab_host="DH108"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invited). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."

BASE COUNT 121 a 202 c 248 g 126 t
ORIGIN

```

Query Match 83.7%; Score 488.2; DB 10; Length 697;
 Best Local Similarity 98.6%; Pred. No. 7.9e-101;
 Matches 345; Conservative 0; Mismatches 3; Indels 5; Gaps 5;

```

Oy 1 atgagcagcccccagcctcgcagccagacacagcagcctgtgtgtgtgtgtgtgtgtgt 60
Db 145 ATGCGACCCAGCAGCTGTGCGCCAGACACAGGGGCTGTGTGTGTGTGTGTGTGTGT 204
Oy 61 aagctgagcagagagagagagagagagagagagagagagagagagagagagagagag 120
Db 205 AAGCTGAGGCGAGAGAGGTTATGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 264
Oy 121 ccgctgcacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
Db 265 CCGCTGCACCAAGCCATGCGGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 324
Oy 181 ttctctgagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 240
Db 325 TTCTGTGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 384
Oy 241 caggtctccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300
Db 385 CAGGCTCCGATGAGACTTTTCAAGGGGGGCCCAACTGGGGCCGCTTGTAGCTTCTTT 444
Oy 301 gtcttgaggctgacactgtgtctgagagtgtaacaagaagatggaaccactgtgtgga 359
Db 445 GTCTTTGGGGGTGCGCTGTGCTGAGAGTGTCAACAAAGAGATGGAACACACTGTGTGG 504
Oy 360 acaagtgcagaagatgagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 418
Db 505 ACAAGTGCAGAGTGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 564
Oy 419 gcaagtggagcgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 477
Db 565 GCAGTGGGGGCTGTGCGGGAGTTCACAGCTATATACAGGGGAGGGGAGGAGGAGGCG 624
Oy 478 cggcgtctcggagagagagagagagagagagagagagagagagagagagagagagag 535
Db 625 CGGCGTGTGAGGGAGGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 684
Oy 536 cactgaggagcct 548
Db 685 CACTGGGGGCGCT 697

RESULT 6 643 bp mRNA linear EST 16-OCT-2001
LOCUS B1910270 603069493f1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5218294 5'
DEFINITION mRNA sequence.
ACCESSION B1910270
VERSION B1910270.1 GI:16173653
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 643)
NIH-MGC http://mhc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM1548 row: j column: 23
High quality sequence stop: 643.
Location/Qualifiers

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source
1. .643
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5218294"
/clone_1lb="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH10B"
/notes="Vector: PCMV-SPORT6; Site.1: NotI; Site.2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned. (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."
129 a 184 c 216 g 114 t

```


Matches 394: Conservative 0; Mismatches 35; Indels 1; Gaps 1;

QY 1 atgggagacccagcctcgcccccagacacacagcgtctgtgtgacagactttagttat 60
 |||||
 Db 112 ATGGGAGACCCCGCTCAACCCAGACAGCGGCTCTAGTGGCTGTGTTGAGCTAT 171
 |||||
 QY 61 aagctgaagcagaaggtatgtctgtgagctgtgccccgggagggccagcagctgac 120
 |||||
 Db 172 AAGCTGAGCGCAAGAGGTTATGTCTGTGAGCTGTGCCCCGGGAGAGGCCAGCGCGGAC 231
 |||||
 QY 121 ccgctgacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
 |||||
 Db 232 CCCTGACACCAAGCATGGGGCTCTGTGAGAGAGTTGAGACCCGTTCCCGCGGACC 291
 |||||
 QY 181 tctctgacatcgtcgagcagcagcagcagcagcagcagcagcagcagcagcagc 240
 |||||
 Db 292 TTCTGTGACCTGTGCGCTCTGCTACAGTGAACCCAGGCTGAGCCAGCAACGCTTAC 351
 |||||
 QY 241 caagctccgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300
 |||||
 Db 352 CAGGTTCCGACCACTTTTCCAGGGGGCCCTTAAGTGGGCGCTGTGAGCAATCTTT 411
 |||||
 QY 301 gtcttgagcgtcagcgtcagcgtcagcgtcagcgtcagcgtcagcgtcagcgtcagc 360
 |||||
 Db 412 GTCTATGGGCTCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGCCTTTGTGGGA 471
 |||||
 QY 361 caagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 420
 |||||
 Db 472 CAACTGCATATGATGATGTGCTGCTGCTGAGAGCAACGCTGCTGAGCTGAT-CACAGC 530
 |||||
 QY 421 agtgggggct 430
 |||||
 Db 531 AGTGGGGCT 540
 |||||

RESULT 11
 B1764428 758 bp mRNA linear EST 25-SEP-2001
 LOCUS 603050701F1 NIH_MGC_116 Homo sapiens CDNA clone IMAGE:5190792 5',
 DEFINITION mRNA sequence.
 ACCESSION B1764428
 VERSION B1764428.1 GI:15756006
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC http://mhc.nci.nih.gov/
 1 (bases 1 to 758)
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov
 Plate: L1M11477 row: a column: 01
 High quality sequence stop: 753.
 Location/Qualifiers
 1..758
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5190792"
 /clone_lib="NIH_MGC_116"
 /lab_host="DH10B"
 /note="Organ: pooled colon, kidney, stomach. Vector:
 pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
 pool anonymous pool of 3 colons, age 26 yo male, 49 yo
 female, 71 yo male colon; 46 yo male kidney, and pool of 2

stomachs, 62 yo male and 70 yo female. library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.4 kb,
 insert size range 1-3 kb. library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 023. Note: this is a NIH-MGC Library."

BASE COUNT 140 a 216 c 228 g 174 t

ORIGIN

Query Match 56.3%, Score 328.4; DB 10; Length 758;
 Best Local Similarity 98.2%; Pred. No. 1.3e-64;
 Matches 332; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 atgggagacccagcctcgcccccagacacacagcgtctgtgtgacagactttagttat 60
 |||||
 Db 139 ATGGGAGACCCCGCTCAACCCAGACAGCGGCTCTAGTGGCTGTGTTGAGCTAT 198
 |||||
 QY 61 aagctgaagcagaaggtatgtctgtgagctgtgccccgggagggccagcagctgac 120
 |||||
 Db 199 AAGCTGAGCGCAAGAGGTTATGTCTGTGAGCTGTGCCCCGGGAGCGCCAGCACTGAC 258
 |||||
 QY 121 ccgctgacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
 |||||
 Db 259 CCCTGACACCAAGCATGGGGCTCTGTGAGAGTGTGAGACCCAGCCCAACAAAGCTTAC 318
 |||||
 QY 181 tctctgacatcgtcgagcagcagcagcagcagcagcagcagcagcagcagcagc 240
 |||||
 Db 319 TTCTGTATGTGCGGCTCTGCTGCTGAGAGTGTCAACAAAGAAATGAGCCTTTGTGGGA 378
 |||||
 QY 241 caagctccgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300
 |||||
 Db 379 CAGGTTCCGACCACTTTTCCAGGGGGCCCTTAAGTGGGCGCTGTGAGCAATCTTT 438
 |||||
 QY 301 gtcttgagcgtcagcgtcagcgtcagcgtcagcgtcagcgtcagcgtcagcgtcagc 360
 |||||
 Db 439 GTCTTGGGCTCGCATGTGCTGCTGAGAGTGTTCAG 476
 |||||

RESULT 12
 BF204905 601 bp mRNA linear EST 06-NOV-2000
 LOCUS 601866718F1 NIH_MGC_17 Homo sapiens CDNA clone IMAGE:4106836 5',
 DEFINITION mRNA sequence.
 ACCESSION BF204905
 VERSION BF204905.1 GI:11098491
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC http://mhc.nci.nih.gov/
 1 (bases 1 to 601)
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaapbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at: image.llnl.gov
 Plate: L1CM987 row: d column: 05
 High quality sequence stop: 561.
 Location/Qualifiers
 1..601
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4106836"
 /clone_lib="NIH_MGC_17"
 /tissue_type="rhodomyosarcoma"

Thu Jun 6 16:39:19 2002

us-09-155-327e-6.rst

Page 12

TITLE Direct Submission
JOURNAL Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and
Eliza Hall Institute of Medical Research, PO Royal Melbourne

FEATURES	Hospital, Parkville, Victoria 3050, Australia
source	location/Qualifiers
	1. .582
	/organism="Homo sapiens"
	/db_xref="taxon:3606"
	/chromosome="14"
	/map="14q11"
gene	1. .582
	/gene="bcl-w"
CDS	1. .582
	/gene="bcl-w"
	/note="promotes cell survival"
	/codon_start=1
	/product="Bcl-w"
	/protein_id="AA09095.1"
	/db_xref="GI:1572493"
	/translation="MATPASAPDTRALVADVEVGYKLRKGYVCGAGFEGEAPADPLHQ
	AMRAGDEFEFRFRRTSDLAOLHIVPGSQOQFFTVSDELPQGGPNORLVAFFVFG
	GAICARSNVMEPELVGOVDEMVAVALLETRLADWIIHSSGMAEFTALYGDGALAEAR
	RLRGKSNVRYVITGVALGVALGALTVAFFPASK"
BASE COUNT	104 a 156 c 211 g 111 t
ORIGIN	

Query Match	99.8%	Score 582;	DB 9;	Length 582;
Best Local Similarity	100.0%	Pred. NO. 4.1e-119;		
Matches 582; Conservative	0;	Mismatches	0;	Indels 0;
		Gaps	0;	

QY	1	atggagaccacccagccctcggccccccagacaagaagcgtctcgtgtgcgaacttgttagttat	60
Db	1	atggacacccacagccctcggccccccagacaacacacggcctcgtgtggccagacttctgttagttat	60
QY	61	aagcttaggcagaagagttatgtctcgttgagcttgcccccgagggaagggccagcagcttacc	120
Db	61	aagcttaggcagaaagggttatgtctcgttgagcttgcccccgagggaagggccacagcacttacc	120
QY	121	ccgctgcaccaagccaatgcgggcagctcggagaatgaattcgaagaccgcttccggcgcaacc	180
Db	121	ccgctgcaccaacaaagccatgcgggcagctcggagaatgagatgattcgagacccttcggcgcaacc	180
QY	181	tctctcgaatctcggcgctcgaagctgaattgaatctgaacccagctcaagcccagacaagcttaacc	240
Db	181	ttctctgaatctcggcgctcgaagctgaattgaatctgaacccagctcaagcccacagccttaacc	240
QY	241	caagctctccgaagaaacttlttcaaaaggggccccaactcggcgccgtgtgaaccttctt	300
Db	241	caggtctccgaagaaacttlttcaaaaggggccccaactcggcgccgtgtgaaccttctt	300
QY	301	gtctttaggggtctgcacctgtgtcgtgagagtgltcaacaagaaatgaaaccactgtgttga	360
Db	301	gtctttaggggtctgcacctgtgtcgtgagagtgltcaacaagaaatgaaaccactgtgttga	360
QY	361	caagtcgaaagatgtgaatgtgttgcctaaccttgaagacgcggtcgtgtgactgtgatccacagc	420
Db	361	caagtcgaaagatgtgaatgtgttgcctaaccttgaagacgcggtcgtgtgactgtgatccacagc	420
QY	421	agtcggggctcgggcgaggtltaacacgctctatacaggggaacggccctcggagagagcgcg	480
Db	421	agtcggggctcgggcgaggttacaacgctctatacaggggaacggccctcggagagagcgcg	480
QY	481	cgtctgcggagggaggaactgtggcctacagtatgagcacaactgcttgacggggggcggtggcactg	540
Db	481	cgtctgcggagggaggaactgtggcctacagtatgagcacaactgcttgacggggggcggtggcactg	540
QY	541	ggggccctgtgaactgtgaaggagcctttttgtctagcaagaatga	582
Db	541	ggggccctgtgaactgtgaaggagcctttttgtctagcaagaatga	582

RESULT	2		
D87461			
LOCUS	D87461	3542 bp	mRNA
DEFINITION	Human mRNA for KIAA0271 gene, complete cds.	linear	PRI 06-OCT-2001

ACCESSION D87461
 VERSION D87461.1 GI:1944417
 KEYWORDS KIAA0271.
 SOURCE Homo sapiens male brain myeloblast cell_line:KG-1 cDNA to mRNA, clone_11b:pspORT 1 clone:HA6752.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 3542)
 AUTHORS Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawarabayasi,Y., Ohara,O., Tanaka,A., Kotani,H., Miyajima,N. and Nomura,N.
 TITLE Prediction of the coding sequences of unidentified human genes. VI. The coding sequences of 80 new genes (KRAA0201-KRAA0280) deduced by analysis of cDNA clones from cell line KG-1 and brain
 JOURNAL DNA Res. 3 (5), 321-329 (1996)
 MEDLINE 97191544
 REFERENCE 2 (bases 1 to 3542)
 AUTHORS Ohara,O., Nagase,T., Kikuno,R. and Nomura,N.
 TITLE Direct Submission
 JOURNAL Submitted (27-AUG-1996) Osamu Ohara, Kazuo DNA Research Institute: 152-3, Yana, Kisanazau, Chiba 297-0812, Japan
 (E-mail:cdnainfo@kazuo.or.jp, Tel:+81-438-52-3913)

FEATURES	Location/Qualifiers
source	1..3542

BASE COUNT	ORIGIN
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a	
817	c
1030	g
891	t

Query Match	99.5%;	Score 579.8;	DB 9;	Length 3542;
Best Local Similarity	99.7%;	Pred. No. 1.1e-118;		
Matches 581; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	1	atggcgaacccacgcttcggccccagaaacacagggctcgtgtgcagactttaggttat	60
Db	177	ATGGCCACCCCGACGCTCGGGCCCGACACACAGGGCTCTGTGTGCACACTTTGTAGTTAT	236
QY	61	aagctgaagcagaagaagtgatctgtctgtgcagctcggccccgggaaggccccagcagctgac	120
Db	237	AAGCTGAGCGACAAGAGTTATGTCTGTGTGAGCTGGCCCCGGGAGGGCCGACAGCTTAC	296
QY	121	cgcctgcacacagacgaatgcgggcagcctcggagatgttgagaaccggttcgcggcgacc	180
Db	297	CGCCTGCACACAGGCAATCGGGGACAGCTGGAGATGATGAGAACCCGGCTTCGGGGCACC	356
QY	181	tctctgtatctcggcgtcagctcagctgcatgtgtaaccacagctcagccacagcagctcaac	240
Db	357	TTCTTGAGTCTGGCGGCTCACTGATGTGACCCAGGCTCAGCCCAACAGCTTCACC	416
QY	241	caggtctccgaagaaactttttcaaggaggccccaaactctggggccgctgtatgctcttc	300
Db	417	CAGGTCTCCGATGAACTTTTCAAGGGGGCCCCAACTGGGGCCGCTGTGACCTTCCTT	476

	301	360	360
OY	gtcttcggagctcactcgtgtgtccgagagtgtaacaagagatgagacacactgtgtgga		
Db	gtctttggggcctgcacctgtgtgtgaagatgtcaacaaggagatggaacacactggttggga	536	
OY	caagtgcagagatgtagtgtgtgtacctagagacgcggtctgtctgactgataccacagc	420	
Db	caatgtcagagagtgtagtgtgtgtacctagagacgcgcgctgtctgactgataccacagc	596	
OY	agtgagggctgtggcgagattcacagctctatacggagacgggagcccttgaaagagcgcg	480	
Db	agtgagggctgtggcgagattcacagctctatacggagacgggagcccttgaaagagcgcg	556	
OY	agtgagggctgtggcgagattcacagctctatacggagacgggagcccttgaaagagcgcg	556	
Db	agtgagggctgtggcgagattcacagctctatacggagacgggagcccttgaaagagcgcg	656	
OY	ctctcgcggagagggaaactgtgcatacagltgaagacaatgtctgaacggggccgtgtgacctg	540	
Db	ctctcgcggagagggaaactgtgcatacagltgaagacaatgtctgaacggggccgtgtgacctg	716	
OY	ggggccctgtgaactgttagggcccttttttctagcaagttaa	583	
Db	ggggccctgtgaactgttagggcccttttttctagcaagttaa	759	

RESULT	3				
AX022529					
LOCUS			583 bp	DNA	Linear
DEFINITION	AX022529				PAT 07-SEP-2000
ACCESSION	Sequence 6 from Patent EP0932674.				
VERSION	AX022529				
KEYWORDS	AX022529.1 GI:10046125				
SOURCE	.				
ORGANISM	unidentified.				
REFERENCE	unclassified.				
AUTHORS	1 (bases 1 to 583)				
TITLE	Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.				
JOURNAL	A novel mammalian gene, bcl-w, belongs to the bcl-2 family of apoptosis-controlling genes Patient: EP 0932674-A 6 04-AUG-1999;				

FEATURES	AMRAD OPERATIONS PTY LTD (AU)
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	/db_xref="GI:10046126"
	/translation="MATPASPDPTRALVDFVGYKLROKGYCGAGPEGCPADPLHT
	ARRAGDEFETRRFRRTFSDLAQLHTTPESAOQRTQVDELFQGGPNMGRIVAFEL
	GALCAESYNKEMKEPLVGQVQEMWVAIETRLVDWTHSSGGMAEFTALYGDALEBA
	RLREGWMAVSRVTLVGCVALGALVTVGAFFASK"
BASE COUNT	105 a 157 c 210 g 111 t
ORIGIN	

Query Match	99.2%	Score 578.2	DB 6	Length 583
Best Local Similarity	99.5%	Pred. No. 2.8e-118		
Matches 580; Conservative	0	Mismatches 3	Indels 0	Gaps 0

QY	1	atggcgcagccacgctctgcgcccccaaacacagggctcttggttgcgaagacttgcattgattc	80
Db	1	ATGGCGCAGCCACGCTCTGGCCCCCAGACACAGGGCTCTGGTGGCAGACTTGTAGGTTAT	60
QY	61	aagctgcagcagaagggtattatctctgtgcagctgcgcgcccggggagggcccaagcagctgcac	120
Db	61	AAGCTGCAGCAGAAGGGTTATGCTGTGGAGACTGGCCCCGGGGAGAGGCCCCAGCAGCTGCAC	120
QY	121	ccgcgtgcacccaagccatgcgcgcgcagctgcgcagatgcgaatgcgaacccgcgtcttcgcgcgaac	180
Db	121	CCGCGTGCACCAAGCCATGCGGGCAGCTGCAGATGAGTTGCGAGACC CGGCTTCGGCGGACC	180
QY	181	ttctctgcattcgcgcgctcagctcgcattgcattgcaccccaagcgtctaagcccaagcaacgcgttaac	240
Db	181	TTCTCTGCATTGCGCGCTCAGCTCGATGATGACCCCAAGGCTCAGGCCCAACAGGCTTCAAC	240

OY	241	caagfctcccgacgaacttltcaaggggcccacaatgaggcgccctltgaagcccttctt	300
Db	241	CAGGCTCCGACGAACCTTTTCAAGGGGGCCCCAACACTGGGGCCCTGTGAGCCTTTT	300
OY	301	gtcctttgggcctgcacgtgtgtcgtgagagtgtaacaagaagatggaaccaatggtgga	360
Db	301	CTCTTTGGGGCTGCACCTGTGTGCTGAGAGTCTCAACAAGAGATGGAAACCACTGTGTGGGA	360
OY	361	caaatgcagagagatgtagtgtgctactcttgagacgcgctgcgtctgtactgataccagc	420
Db	361	CAAGTGCAGAGATGATGATGTGTGTGCTGAGAGACGCGGTGTCGACTGTGATCCACAGC	420
OY	421	agtggaggactggcggagatltcaagcttcatacgggagcggccctggaggaagcgcg	480
Db	421	AGTGGGGGCTGGCGGAGTTCACACCTTTAAACGGGGACGGGGCCCTGGAGAGGGCGGG	480
OY	481	cgctcgcggagaggaactgggcctacatggaggaagatgctgcagacgggggcgttgcactg	540
Db	481	CCTTCGCGGAGGGAACCTGGGCATCAGTAGAGACAGTGTACCGGGGCCGTGGCACTG	540
OY	541	ggggccctgtaactgttaaggccttlttggtaagaaatgaa	583
Db	541	GGGGCCCTGTAACTGTATAGGGCCCTTTTTCCTACCAAGTGA	583

RESULT	4				
AX030817					
LOCUS	AX030817	583 bp	DNA	linear	PAT 20-SEP-2000
DEFINITION	Sequence 6 from Patent WO935571.				
ACCESSION	AX030817				
VERSION	AX030817.1	GI:10278311			
KEYWORDS					
SOURCE	unidentified.				
ORGANISM	unidentified.				
	unclassified.				
REFERENCE	1 (bases 1 to 583)				
AUTHORS	Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.				
TITLE	A novel mammalian gene, bcl-w, belongs to the bcl-2 family of apoptosis-controlling genes				
JOURNAL	Patent: WO 9735971-A 6 02-OCT-1997;				

```

FEATURES
    source
        ADAMS JERRY MCEE (AU) ; HOLMGREEN SHAWN F (AU) ; CORA SEANANNE (AU)
        ; GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)
            location/Qualifiers
                1..583
            /organism="unidentified"
            /db_xref="taxon:32644"
            1..583
            /note="unnamed protein product"
            /codon_start=1
            /protein_id="CAC09621.1"
            /db_xref="gi:10278312"
            /translation="MATPSADPRTALVADFPYGIKLRQKGYCGAGPGEGPADPLH
            AMGAADDEFETRRRTFSDLAQLHVTSPSAQORFTQVSDLELPQGPNNKGRIVAFPL
            GALCAESVNRKEPLVGOVQOEVMVAVILETRVLVDWIHSSGGAPEFTALYGDGALBEAA
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BASE COUNT
    105 a
    157 c
    210 g
    111 t

ORIGIN

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[illegible]

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181 |ttctcgtatcgtgagcgtacgtcgtgtgacccagcgtcagccagcagcgtcacc|
181 |ttctcgtatcgtgagcgtacgtcgtgtgacccagcgtcagccagcagcgtcacc|
241 |caaggtccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc|
241 |CAGGTCTCCGAGCACTTTTCAAGGGGGCCCCCACTGGGGGGCGCTTGTACCTTTT|
301 |gtcttggggtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc|
301 |CCTTTGGGGGCTGCACTGTGTCTGAGACTGTCAACAGAGATGAAACCACTGCTGGA|
361 |caagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc|
361 |CAAGTGCAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT|
421 |agtgagcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc|
421 |AGTGGGGGCTGGCGGAGTTCACAGCTCTATACGGGGGAGCGGGCTGAGAGAGCGGG|
481 |cgtctcgggagggagggagggagggagggagggagggagggagggagggagggaggg|
481 |CCTTTCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG|
541 |ggggccttgtagttagttagttagttagttagttagttagttagttagttagttagt|
541 |GGGGCCCTGTGTAAGTGTAGGGGCTTTTCTGTAGCAAGTGA 583

```

RESULT 5
BC021198
LOCUS BC021198 1437 bp mRNA linear PRI 22-JAN-2002
DEFINITION Homo sapiens, BCL2-like 2, clone MGC:10675 IMAGE:3944307, mRNA,
complete cds.
ACCESSION BC021198
VERSION BC021198.1 GI:18203706
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1437)
Strausberg, R.
Direct Submission
Submitted (14-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cga@r-email.nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nih.gov
Shenoy, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.M., Bouffard, G.G., Brinkley, C., Brooks, S.,
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, G.L., Mastello, C., Mastrian, S.D., McCloskey, D.C.,
McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J.,
Tiongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-R. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
Series: IRML Plate: 15 Row: K Column: 19

FEATURES
source This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 14574571.
1. 1437
Location/Qualifiers

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/db_xref="taxon:9606"
/db_xref="LocusID:599"
/clone="MGC:10675 IMAGE:3944307"
/tissue="lung, small cell carcinoma"
/clone_id="NIH-MGC-7"
/lab_host="DH10B-R"
/note="Vector: pORF7"
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/codon_start=1
/product="BCL2-like 2"
/protein_id="AAH21198.1"
/db_xref="GI:18203707"
/translation="MATPASPAPDTRALVDFVGYKLRGKYVYAGAGPREGPAPDLHO
AMRAGDEFETRRFRFSLADLHVTTPSAAQRTQVSDLPQGGPMGRVAFVF
GALCESVKNKEPVLGVQEMVATLETRLDLHSHSGMAEFTALYDGALEEAR
RLREGMAVSRVLTGAVLGLVGAFAFSK"

BASE COUNT 303 a 343 c 509 g 282 t
ORIGIN

Query Match 99.2% Score 578.2; DB 9; Length 1437;
Best Local Similarity 99.5%; Pred. No. 2, 6e-118;
Matches 380; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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176 ATGAGCAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC
235
61 aagctgaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc
236 AAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
295
121 ccgctgacacacacacacacacacacacacacacacacacacacacacacacacacacacacac
296 CCAGTGCAGCAAGCCATGCGGGGAGTGCAGATGAGTGCAGATGAGTGCAGATGAGTGCAG
355
181 ttctcgtatcgtgagcgtacgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc
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241 caagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc
416 CAGGTCTCCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT
475
301 gtcttggggtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc
476 GTCTTGGGGGCTGCACTGTGTCTGAGACTGTCAACAGAGATGAAACCACTGCTGGA
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536 CAAGTGCAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT
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421 agtgagcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc
596 AGTGGGGGCTGGCGGAGTTCACAGCTCTATACGGGGGAGCGGGCTGAGAGAGCGGG
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481 cgtctcgggagggagggagggagggagggagggagggagggagggagggagggagggaggg
656 CGTCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
715
541 ggggccttgtagttagttagttagttagttagttagttagttagttagttagttagt
716 GGGGCCCTGTGTAAGTGTAGGGGCTTTTCTGTAGCAAGTGA 758

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RESULT 6
AR020780 AR020780 579 bp DNA linear PART 05-DEC-1998
LOCUS

DEFINITION Sequence 2 from patent US 5789201.
 ACCESSION AR020780
 VERSION AR020780.1 GI:3975395
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 579)
 AUTHORS Guastella, J.
 TITLE Genes coding for bcl-2 and bcl-2 homologues
 JOURNAL Patent: US 5789201-A 2.04-AVG-1998;
 FEATURES Location/Qualifiers
 source 1..579
 /organism="unknown"
 BASE COUNT 106 a 154 c 208 g 111 t
 ORIGIN

Query Match 98.2%; Score 572.6; DB 6; Length 579;
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 Matches 575; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 atggcagcccccagcctcgccgcccagacacacagcggcctctggtggaagcattgttgat 60
 Db 1 ATGGCAGCCCCAGCCTCGCGCCCGCCAGACACAGCGGCTCTGTTGGAAGCTTGTAGGTTAT 60

QY 61 aagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 120
 Db 61 AAGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 120

QY 121 ccgctgacccacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
 Db 121 CCAGCTGACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 180

QY 121 ccactgcac 180
 Db 121 CCAGCTGACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 180

QY 181 ttctctgac 240
 Db 181 TTCTCTGACCTCGCGGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTC 240

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 Db 241 CAGCTCTCCGAGTAACTTTTTCAGAGGGGGCCCCCAACTGGGGGCTTGTAGCTTCTTT 300

QY 301 gctcttgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 360
 Db 301 GCTCTTGAGGCTGACCTGT 360

QY 361 caagctcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 420
 Db 361 CAACTGACAGGAGT 420

QY 421 agtggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480
 Db 421 AGTGGAGGCTGGGCGGAGTTCACAGCTCTATACGGGGGAGGGGCTTGTAGAGAGCGGG 480

QY 481 cgtctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 540
 Db 481 CGTCTGCGGAGGAGGAGT 540

QY 541 ggggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 579
 Db 541 GGGGAGCCTGT 579

RESULT 7
 AF096291 AF096291 582 bp mRNA linear ROD 28-FEB-2000
 LOCUS Rattus norvegicus Bcl-2 (bcl-2) mRNA, complete cds.
 DEFINITION AF096291
 ACCESSION AF096291.1 GI:3747129
 VERSION AF096291.1
 KEYWORDS Norway rat.
 SOURCE Rattus norvegicus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 582)
 AUTHORS Hammer, S., Skogjosa, Y. and Lindholm, D.
 TITLE Differential expression of bcl-2 and bcl-2 messenger RNA in the developing and adult rat nervous system
 JOURNAL Neuroscience 91 (2), 673-684 (1999)
 MEDLINE 99292146
 PUBMED 10366024
 REFERENCE 2 (bases 1 to 582)
 AUTHORS Hammer, S., Skogjosa, Y. and Lindholm, D.
 TITLE Direct Submission
 JOURNAL Submitted (01-OCT-1998) Developmental Neuroscience, Uppsala University, Box 587, BMC, Uppsala 751 23, Sweden
 FEATURES Location/Qualifiers
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 LRAAGDETERFRFTSDLAQLHVTGSGAQQRPTQSDLPFGPMMGLVAFV
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 RLRENNMASVRLVGLGVALGLVGFVAFASK"

BASE COUNT 111 a 157 c 200 g 114 t
 ORIGIN

Query Match 91.3%; Score 532.4; DB 10; Length 582;
 Best Local Similarity 94.7%; Pred. No. 4.1e-108;
 Matches 551; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 atggcagcccccagcctcgccgcccagacacacagcggcctctggtggaagcattgttgat 60
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 Db 61 AAGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 120

QY 121 ccgctgacccacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
 Db 121 CCAGCTGACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 180

QY 121 ccgctgacccacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
 Db 121 CCAGCTGACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 180

QY 181 ttctctgac 240
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QY 301 gctcttgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 360
 Db 301 GCTCTTGAGGCTGACCTGT 360

QY 361 caagctcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 420
 Db 361 CAACTGACAGGAGT 420

QY 421 agtggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480
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gene
1. .3476
/gene="Bcl-w"
exon
1. .82
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83. .170
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179. .760
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[illegible]

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RESULT 11
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LOCUS AX022531 581 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 8 from Patent EP0932674.
ACCESSION AX022531
VERSION AX022531.1 GI:10046127
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.
TITLE A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
apoptosis-controlling genes
Patent: EP 0932674-A 8 04-AUG-1999;
AMRAD OPERATIONS PTY LTD (AU)
JOURNAL location/Qualifiers
FEATURES
SOURCE 1..581

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KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Mammalia: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 196292)
AUTHORS Heilig, R., Petit, J. L., Vilco, V., Dasilva, C., Robert, C., Mueker, P.,
Bottler, P., Cattoico, L., Barbe, V., Pelletier, E., Artiguenave, F.,
Levy, M., Eckenberg, R., Bruls, T., deherardis, V., Cruaud, C.,
Gyapay, G., Saurin, W., and Weissbach, J.
TITLE Sequencing of the human chromosome 14
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 196292)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (21-MAY-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT On Jun 3, 2000 this sequence version replaced gi:6138746.
----- Genome Center
Center: Genoscope / Centre National de Sequencage
Center code: GS
Web site: http://www.genoscope.cns.fr/
Contact: Seqref@genoscope.cns.fr

The following BAC sequence is oriented from the T7 to the SP6 end.
Upstream BAC (overlapping the T7 end) : R-244E17
Downstream BAC (overlapping the SP6 end) : C-2201G16 (AC-AL132855)
----- Summary Statistics
Assembly program: Phrap; version 2.0
Quality coverage: 7.94x in Q20 bases; sum-of-contigs

Overall quality chart :

Range : bases
0 - 9 :
1 - 9 :
10 - 19 :
20 - 29 :
30 - 39 :
40 - 49 :
50 - 59 :
60 - 69 :
70 - 79 :
80 - 89 :
90 - 99 :
111256

Percentage of bases with a quality value >= 40 : 99 %

FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
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/chromosome="14"
/clone="R-124D2"
/clone_lib="RPC1-11"
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RHD:RH102162
dbSTS:STS69699
Identified using the e-PCR software (G. Schuler)"
STS
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RHD:RH98727
dbSTS:STS68485
Identified using the e-PCR software (G. Schuler)"
STS
82164..82299
/note="matching EMBL:H79035
RHD:RH76773
dbSTS:STS53514
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RHD:RH75103

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dbSTS:STS25817
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128419..128543
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RHD:RH53698
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RHD:RH28671
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138805..138926
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161617..161761
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RHD:RH92419
dbSTS:STS65422
Identified using the e-PCR software (G. Schuler)"
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dbSTS:STS53407
Identified using the e-PCR software (G. Schuler)"
BASE COUNT 50870 a 45673 c 47123 g 52626 t
ORIGIN
Query Match 73.4%; Score 428.2; DB 9; Length 196292;
Best Local Similarity 99.3%; Pred No.3;le-85;
Matches 430; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 atggcgagccagcctgcgcccagacagagggctctgtgtgagacttttaggtat 60
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Db 89826 ATGGCGAGCCAGCCTGCGCCAGACACAGCGGCTGTGTGAGACTTTTAgGTTAT 89885
QY 61 aagctgagcgagaaagggtatgtctgtgagagctgagcccgagagagggccagcagctgac 120
|||||
Db 89886 AAGCTGAGCGCAGAGGGGTTATGTCTGTGTGAGAGTGGCCCGGAGGAGGCCAGAGCTGAC 89945

Thu Jun 6 16:39:17 2002

us-09-155-327e-6.rge

Page 12

DR WPI; 1997-489635/45.
DR P-PSDB; AAM36047.

XX Nucleic acid encoding apoptosis related gene bcl-w - used to induce
PT or inhibit cell survival, e.g. for treatment of cancer and
PT degenerative diseases
XX

PS Claim 3: Page 48; 86pp; English.

XX This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene
CC family, extracted from an adult brain library. This gene promotes cell
CC survival, so its modulation is useful in treatment of cancer or
CC auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's
CC disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia,
CC human immunodeficiency virus infection or in cell transplants,
CC Up-regulation of the gene can also be used to modify cell lines cultured
CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas
CC and to increase survival of primary explants during genetic modification.
CC It can be used to produce recombinant Bcl-w for therapy, diagnosis,
CC antibody production or screening of potential modulators.
XX

SQ Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;

Query Match 99.2%; Score 578.2; DB 18; Length 583;
Best Local Similarity 99.5%; Pred. No. 3e-134;
Matches 580; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 1 atggcaccacagcctcggccacagacacagcgtctgtgtgacagctttagttat 60
OY 61 aagctgaagcagaaggggtatgtctgtgagctgcccggaggagggccagcagctgac 120
Db 61 aagctgaagcagaaggggtatgtctgtgagctgcccggaggagggccagcagctgac 120
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Db 121 ccgctgacacaaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
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Db 241 caagctccagcagaacttttcaaggaggcccaactgtggccgctgtgactcttctt 300
OY 301 gtcttgggagcgtcagcgtcagcgtcagcgtcagcgtcagcgtcagcgtcagcgtc 360
Db 301 gtcttgggagcgtcagcgtcagcgtcagcgtcagcgtcagcgtcagcgtcagcgtc 360
OY 361 caagctcagaagtgagtggtggtggtggtggtggtggtggtggtggtggtggtggtg 420
Db 361 caagctcagaagtgagtggtggtggtggtggtggtggtggtggtggtggtggtggtg 420
OY 421 agtgggagcgtcagcgtcagcgtcagcgtcagcgtcagcgtcagcgtcagcgtcagc 480
Db 421 agtgggagcgtcagcgtcagcgtcagcgtcagcgtcagcgtcagcgtcagcgtcagc 480
OY 481 cgtctcagcagaagggagtgatgtctgtgagcgtcggcgagcgtcggcgagcgtcgg 540
Db 481 cgtctcagcagaagggagtgatgtctgtgagcgtcggcgagcgtcggcgagcgtcgg 540
OY 541 ggggcccctgtaactgtatgggccccttttctgtagcaagtga 583
Db 541 ggggcccctgtaactgtatgggccccttttctgtagcaagtga 583
```

RESULT 2
AAX25134
ID AAX25134 standard; DNA; 583 BP.
XX

```
AC AAX25134;
XX
XX 05-JUL-1999 (first entry)
XX
XX Human bcl-w gene derivative.
XX
XX Spermatoogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
XX animal model; ss.
XX
XX Homo sapiens.
XX
XX WO9913710-A1.
XX
XX 25-MAR-1999.
XX
XX 16-SEP-1998; 98WO-AU00764.
XX
XX 16-SEP-1997; 97AU-0009228.
XX
XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
XX Adams J, Cory S, Gibson L, Koentgen F, Print C;
XX
XX WPI; 1999-243890/20.
XX
XX P-PSDB; AAY05532.
XX
XX An animal model exhibiting reduced levels of a Bcl-w protein and/or
XX protein associated with Bcl-w
XX
XX Disclosure; Page 36; 52pp; English.
```

The present sequence is described as a derivative of the human bcl-w gene (see AAX25132) and encodes Bcl-w protein (see AAY05532), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation in at least one allele of the human or murine bcl-w gene or in a gene associated with bcl-w. Such animals have disorganised seminiferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility.

SQ Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;

Query Match 99.2%; Score 578.2; DB 20; Length 583;
Best Local Similarity 99.5%; Pred. No. 3e-134;
Matches 580; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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OY 1 atggcaccacagcctcggccacagacacagcgtctgtgtgacagctttagttat 60
Db 1 atggcaccacagcctcggccacagacacagcgtctgtgtgacagctttagttat 60
OY 61 aagctgaagcagaaggggtatgtctgtgagcgtcggcgaggagggccagcagctgac 120
Db 61 aagctgaagcagaaggggtatgtctgtgagcgtcggcgaggagggccagcagctgac 120
OY 121 ccgctgacacaaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
Db 121 ccgctgacacaaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
OY 181 ttctctgatctgagcgtcagcgtcagcgtcagcgtcagcgtcagcgtcagcgtcagcgtc 240
Db 181 ttctctgatctgagcgtcagcgtcagcgtcagcgtcagcgtcagcgtcagcgtcagcgtc 240
OY 241 caagctccagcagaacttttcaaggaggcccaactgtggccgctgtgactcttctt 300
```

```

Db      241 caggtctccgcagcaacttttccaaggcgcccaactgaggccgcttgagcctctt 300
        |||
Oy      301 gtcttggggcgcagctgtgtcgtgagagtgcaacaagagatggaaccactggtggga 360
        |||
Db      301 cctcttggggcgcagctgtgtcgtgagagtgcaacaagagatggaaccactggtggga 360
        |||
Oy      361 caagtcgagagatgagatgtgtgtccttaactgagacgcggctgctgtgactgataccacagc 420
        |||
Db      361 caagtcgagagatgagatgtgtgtccttaactgagacgcggctgctgtgactgataccacagc 420
        |||
Oy      421 agtggggcgtgagcgagatcacaagctctatacggggacgggcccctggagagcgcg 480
        |||
Db      421 agtggggcgtgagcgagatcacaagctctatacggggacgggcccctggagagcgcg 480
        |||
Oy      481 cgtctcgagagaggaactggtgacatagagagcagtgctgacggggccgtgtgacactg 540
        |||
Db      481 cgtctcgagagaggaactggtgacatagagagcagtgagacagtcgacggggccgtgtgacactg 540
        |||
Oy      541 ggggcccctgtaactgtaaggccttttctgctagcaagtga 583
        |||
Db      541 ggggcccctgtaactgtaaggccttttctgctagcaagtga 583
        |||

```

RESULT 3

AAV25132 standard; DNA; 581 BP.

ID AAV25132:

AC AAV25132:

XX 05-JUL-1999 (first entry)

XX 05-JUL-1999 (first entry)

XX 05-JUL-1999 (first entry)

XX 05-JUL-1999 (first entry)

XX 05-JUL-1999 (first entry)

XX 05-JUL-1999 (first entry)

XX 05-JUL-1999 (first entry)

XX 05-JUL-1999 (first entry)

XX 05-JUL-1999 (first entry)

XX 05-JUL-1999 (first entry)

XX 05-JUL-1999 (first entry)

XX 05-JUL-1999 (first entry)

XX 05-JUL-1999 (first entry)

XX 05-JUL-1999 (first entry)

XX 05-JUL-1999 (first entry)

XX 05-JUL-1999 (first entry)

XX 05-JUL-1999 (first entry)

XX 05-JUL-1999 (first entry)

XX 05-JUL-1999 (first entry)

XX 05-JUL-1999 (first entry)

XX 05-JUL-1999 (first entry)

XX 05-JUL-1999 (first entry)

XX 05-JUL-1999 (first entry)

inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility.

Query Match 99.1%; Score 577.8; DB 20; Length 581; Best Local Similarity 99.7%; Pred. No. 3.7e-134; Matches 579; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Oy      1 atgagcaccacagcctcgccccaagacacacagcctgtgtgcaagactttagattat 60
        |||
Db      1 atgagcaccacagcctcgccccaagacacacagcctgtgtgcaagactttagattat 60
        |||
Oy      61 aagtcgagcagaaaggtatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 120
        |||
Db      61 aagtcgagcagaaaggtatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 120
        |||
Oy      121 ccgctgacacacagcctcgccccaagacacacagcctgtgtgacccgcttccggcgac 180
        |||
Db      121 ccgctgacacacagcctcgccccaagacacacagcctgtgtgacccgcttccggcgac 180
        |||
Oy      181 tctctgacatcgccgctcagctgacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 240
        |||
Db      181 tctctgacatcgccgctcagctgacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 240
        |||
Oy      241 caggtctccgcagcaacttttccaaggcgcccaactgaggcgccgtgtgagcctctt 300
        |||
Db      241 caggtctccgcagcaacttttccaaggcgcccaactgaggcgccgtgtgagcctctt 300
        |||
Oy      301 gtcttggggcgcagctgtgtcgtgagagtgcaacaagagatggaaccactggtggga 360
        |||
Db      301 gtcttggggcgcagctgtgtcgtgagagtgcaacaagagatggaaccactggtggga 360
        |||
Oy      361 caagtcgagagatgagatgtgtgtccttaactgagacgcggctgctgtgactgataccacagc 420
        |||
Db      361 caagtcgagagatgagatgtgtgtccttaactgagacgcggctgctgtgactgataccacagc 420
        |||
Oy      421 agtggggcgtgagcgagatcacaagctctatacggggacgggcccctggagagcgcg 480
        |||
Db      421 agtggggcgtgagcgagatcacaagctctatacggggacgggcccctggagagcgcg 480
        |||
Oy      481 cgtctcgagagaggaactggtgacatagagagcagtgctgacggggccgtgtgacactg 540
        |||
Db      481 cgtctcgagagaggaactggtgacatagagagcagtgctgacggggccgtgtgacactg 540
        |||
Oy      541 ggggcccctgtaactgtaaggccttttctgctagcaagtga 581
        |||
Db      541 ggggcccctgtaactgtaaggccttttctgctagcaagtga 581
        |||

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RESULT 4

AAV28334 standard; cDNA; 579 BP.

ID AAV28334:

AC AAV28334:

XX 02-OCT-1998 (first entry)

XX 02-OCT-1998 (first entry)

XX 02-OCT-1998 (first entry)

XX 02-OCT-1998 (first entry)

XX 02-OCT-1998 (first entry)

XX 02-OCT-1998 (first entry)

XX 02-OCT-1998 (first entry)

XX 02-OCT-1998 (first entry)

XX 02-OCT-1998 (first entry)

XX 02-OCT-1998 (first entry)

XX 02-OCT-1998 (first entry)

Key Location/Qualifiers
1..579
/*tag= a
/product= bcl-y
/note= "No stop codon given"

US5789201-A.

PD 04-AUG-1998.
 XX
 XX 11-FEB-1997; 97US-0798897.
 XX
 XX 23-FEB-1996; 96US-0012201.
 PR 11-FEB-1997; 97US-0798897.
 XX
 XX (COCE-) COCENSYS INC.
 PA
 XX Guastella J;
 PI
 XX WPI: 1998-446079/38.
 DR P-PSDB; AAM61392.
 XX
 XX Nucleic acids encoding B-cell lymphoma-Y protein - useful for
 PT producing recombinant protein for use in treating uncontrolled cell
 PT growth e.g. cancers
 XX
 XX Claim 3; Column 15/16; 27pp; English.
 PS
 CC The mammalian bcl-y genes encode a protein that is a member of the bcl-2
 CC family, components in the cell death pathway. The bcl-2 family
 CC have both apoptotic activity and the apoptosis blocking activity. bcl-y
 CC falls in the apoptosis activity category. The recombinant protein may
 CC be used to prevent uncontrolled cell growth, either by its direct
 CC administration to recombinant genetic constructs to increase its
 CC expression in vivo. Also, antisense constructs can be used in disorders
 CC where prevention of cell death is desired.
 XX
 XX Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;

Query Match 98.2%; Score 572.6; DB 19; Length 579;
 Best Local Similarity 99.3%; Pred. No. 7.2e-133;
 Matches 575; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 atggagaccacagctcgccacagacacagggctctgtgtgcaagatttgaattat 60
 DB 1 atggagaccacagctcgccacagacacagggctctgtgtgcaagatttgaattat 60
 QY 61 aagctgagcagaaggattatgtctgtgagctgagcccgaggagggcccaagactgac 120
 DB 61 aagctgagcagaaggattatgtctgtgagctgagcccgaggagggcccaagactgac 120
 QY 121 ccgctgacacaaagcagatcgagcagctgagatgattcgagccgcttcggcgacc 180
 DB 121 ccgctgacacaaagcagatcgagcagctgagatgattcgagccgcttcggcgacc 180
 QY 181 ttctctgactgagctcagctgacatgataccacagccagccacagacagcttcacc 240
 DB 181 ttctctgactgagctcagctgacatgataccacagccagccacagacagcttcacc 240
 QY 241 caggtcccgacgaacttttcaaggggcccaactggggcgccctgttagcctctt 300
 DB 241 caggtcccgacgaacttttcaaggggcccaactggggcgccctgttagcctctt 300
 QY 301 gtcttggagctgcacgtgtgtgtgagatgtcaacaagaatggaatgaacactgtgtgga 360
 DB 301 gtcttggagctgcacgtgtgtgtgagatgtcaacaagaatggaatgaacactgtgtgga 360
 QY 361 caagtgcaagagatgtagtgbgcttacctgagagacggcgctgctgactgataccacagc 420
 DB 361 caagtgcaagagatgtagtgbgcttacctgagagacggcgctgctgactgataccacagc 420
 QY 421 agtgggggcttggcgagatcacaagctatatacgggagcggccctgagagagcgcg 480
 DB 421 agtgggggcttggcgagatcacaagctatatacgggagcggccctgagagagcgcg 480
 QY 481 cgtctcgagagagagactggtgcatcagtggaagacagctgtaacggggcgctgtgcaactg 540
 DB 481 cgtctcgagagagagactggtgcatcagtggaagacagctgtaacggggcgctgtgcaactg 540
 QY 541 gggggcctgtgtaactgtagggcctttttgttagcaag 579

DB 541 gggggcctgtgtaactgtagggcctttttgttagcaag 579

RESULT 5
 ID AAX15946
 AAX15946 standard; CDNA; 579 BP.

AAX15946;

20-MAY-1999 (first entry)

CDNA encoding the human bcl-y protein.

Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
 programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
 head trauma; Alzheimer's disease; neural; muscular degenerative disease;
 multiple sclerosis; myocardial infarction; vitally induced cell death;
 aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
 premature cell death; cell death stimulator; prolonged cell life span;
 Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
 parasite; ss.

Homo sapiens.

US583229-A.

16-MAR-1999.

25-NOV-1997; 97US-0978523.

23-FEB-1996; 96US-0012201.

11-FEB-1997; 97US-0798897.

25-NOV-1997; 97US-0978523.

(COCE-) COCENSYS INC.

Guastella J;

WPI: 1999-214150/18.

P-PSDB; AAM97392.

Novel bcl-y homologues of the rat and human bcl-2 protein - useful
 for modulating programmed cell death

Disclosure; Columns 15-16; 26pp; English.

The present sequence encodes human bcl-y protein (Hbcl-y). The
 specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and
 Hbcl-y are homologues of the bcl-2 protein thought to be involved in
 programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
 proteins may be used to treat conditions associated with a disruption of
 the cell death pathway. If they act as cell death inhibitors, they may be
 used in therapies to treat subjects suffering from: strokes, head trauma,
 Alzheimer's disease, neural and muscular degenerative diseases
 (especially multiple sclerosis), myocardial infarction, vitally induced
 cell death, aging, spinal cord injuries and amyotrophic lateral
 sclerosis- conditions where cells under go premature cell death as a
 result of triggers which may or may not be apparent. They may also be
 used in this way to develop cell lines which remain viable in culture for
 an extended period. In contrast, if they act as cell death stimulators,
 Rbcl-y and Hbcl-y may be used to treat conditions associated with
 prolonged cell life span such as cancer (especially Kaposi's sarcoma and
 lung cancer) and auto/hyperimmune diseases. They may also be used to
 cause cell death in, and hence control, parasites.

Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;

Query Match 98.2%; Score 572.6; DB 20; Length 579;
 Best Local Similarity 99.3%; Pred. No. 7.2e-133;
 Matches 575; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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OY 1 atgagcagcccccagctcgcccccagacacagggctctgtgtgagagactttagtatt 60
    |||
DB 1 atgagcagcccccagctcgcccccagacacagggctctgtgtgagagactttagtatt 60
OY 61 aagctgagcagaaagaggtatgtctgtgagctgccccggggagggccagcagctgac 120
    |||
DB 61 aagctgagcagaaagaggtatgtctgtgagctgccccggggagggccagcagctgac 120
OY 121 ccgctgcacacagcagctcgaggcagctgagatgattcggagaccggttcggcgacac 180
    |||
DB 121 ccagctgcacacagcagctcgaggcagctgagatgattcggagaccggttcggcgacac 180
OY 181 ttctctgagatctgagcagctgagctgagctgagctgagctgagctgagctgagctgac 240
    |||
DB 181 ttctctgagatctgagcagctgagctgagctgagctgagctgagctgagctgagctgac 240
OY 241 caagctcgcagcagactttttcaagggggcccccaactggcgccgtcttgagcttctt 300
    |||
DB 241 caagctcgcagcagactttttcaagggggcccccaactggcgccgtcttgagcttctt 300
OY 301 gtctttgggctgctgactgtgtgtgagagatgtcaacaagagatgaaacactgtgtgga 360
    |||
DB 301 gtctttgggctgctgactgtgtgtgagagatgtcaacaagagatgaaacactgtgtgga 360
OY 361 caagtgacagagatgagatgtgtgagctgagcagcagcagcagcagcagcagcagcagc 420
    |||
DB 361 caagtgacagagatgagatgtgtgagctgagcagcagcagcagcagcagcagcagcagc 420
OY 421 agtgaggagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480
    |||
DB 421 agtgaggagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480
OY 481 agtgaggagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 540
    |||
DB 481 agtgaggagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 540
OY 541 ggggcccctgtgactgtgtgagggcctttttgctagcaag 579
    |||
DB 541 ggggcccctgtgactgtgtgagggcctttttgctagcaag 579

RESULT 6
AAV28333
ID AAV28333 standard: cDNA: 579 BP.
XX
AC AAV28333:
XX
DT 02-OCT-1998 (first entry)
XX
DE Rat bcl-y gene.
XX
KW ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..579
FT /tag= a
FT /product= bcl-y
FT /note="No stop codon given"
XX
XX US5789201-A.
XX
XX PD 04-AUG-1998.
XX
XX PF 11-FEB-1997; 97US-0798897.
XX
XX PR 23-FEB-1996; 96US-0012201.
XX
XX PR 11-FEB-1997; 97US-0798897.
XX
XX PA (COCE-) COCENSYS INC.
XX
XX PI Guastella J;
```

```
XX
DR WPI: 1998-446079/38.
DR P-PSDB: AAM61391.
XX
PT Nucleic acids encoding B-cell lymphoma-Y protein - useful for
PT producing recombinant protein for use in treating uncontrolled cell
PT growth e.g. cancers
XX
PS Claim 2: Column 13/14; 27pp; English.
XX
XX The mammalian bcl-y genes encode a protein that is a member of the bcl-2
XX family, components in the cell death pathway. The bcl-2 family
XX have both apoptotic activity and the apoptosis blocking activity. bcl-y
XX falls in the apoptosis activity category. The recombinant protein may
XX be used to prevent uncontrolled cell growth, either by its direct
XX administration to recombinant genetic constructs to increase its
XX expression in vivo. Also, antisense constructs can be used in disorders
XX where prevention of cell death is desired.
XX
XX Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 other;
XX
XX
XX Query Match 90.5%; Score 527.8; DB 19; Length 579;
XX Best Local Similarity 94.5%; Pred. No. 9, 6e-122;
XX Matches 547; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
XX
OY 1 atgagcagcccccagctcgcccccagacacagggctctgtgtgagagactttagtatt 60
    |||
DB 1 atgagcagcccccagctcgcccccagacacagggctctgtgtgagagactttagtatt 60
OY 61 aagctgagcagaaagaggtatgtctgtgagctgccccggggagggccagcagctgac 120
    |||
DB 61 aagctgagcagaaagaggtatgtctgtgagctgccccggggagggccagcagctgac 120
OY 121 ccgctgcacacagcagctcgaggcagctgagatgattcggagaccggttcggcgacac 180
    |||
DB 121 ccgctgcacacagcagctcgaggcagctgagatgattcggagaccggttcggcgacac 180
OY 181 ttctctgagatctgagcagctgagctgagctgagctgagctgagctgagctgagctgac 240
    |||
DB 181 ttctctgagatctgagcagctgagctgagctgagctgagctgagctgagctgagctgac 240
OY 241 caagctcgcagcagactttttcaagggggcccccaactggcgccgtcttgagcttctt 300
    |||
DB 241 caagctcgcagcagactttttcaagggggcccccaactggcgccgtcttgagcttctt 300
OY 301 gtctttgggctgctgactgtgtgtgagagatgtcaacaagagatgaaacactgtgtgga 360
    |||
DB 301 gtctttgggctgctgactgtgtgtgagagatgtcaacaagagatgaaacactgtgtgga 360
OY 361 caagtgacagagatgagatgtgtgagctgagcagcagcagcagcagcagcagcagcagc 420
    |||
DB 361 caagtgacagagatgagatgtgtgagctgagcagcagcagcagcagcagcagcagcagc 420
OY 421 agtgaggagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480
    |||
DB 421 agtgaggagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480
OY 481 agtgaggagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 540
    |||
DB 481 agtgaggagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 540
OY 541 ggggcccctgtgactgtgtgagggcctttttgctagcaag 579
    |||
DB 541 ggggcccctgtgactgtgtgagggcctttttgctagcaag 579

RESULT 7
AAV15945
ID AAV15945 standard: cDNA: 579 BP.
XX
AC AAV15945:
```

20-MAY-1999 (first entry)
 XX XX
 DE cDNA encoding the rat bcl-2 protein.
 XX XX
 KW Rat bcl-2 protein; Rbcl-2; human bcl-2 protein; Hbcl-2; bcl-2 homologues;
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
 KW head trauma; Alzheimer's disease; neural; muscular degenerative disease;
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
 KW premature cell death; cell death stimulator; prolonged cell life span;
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
 KW parasite; ss.
 XX XX
 OS Rattus sp.
 XX XX
 PN US5883229-A.
 XX XX
 PD 16-MAR-1999.
 XX XX
 PF 25-NOV-1997; 97US-0978523.
 XX XX
 PR 23-FEB-1996; 96US-0012201.
 PR 11-FEB-1997; 97US-0798897.
 PR 25-NOV-1997; 97US-0978523.
 XX XX
 PA (COCE-) COCENSYS INC.
 XX XX
 PI Guastella J;
 XX XX
 DR WPI; 1999-214150/18.
 DR P-PSDB; AAW97391.
 XX XX
 PT Novel bcl-2 homologues of the rat and human bcl-2 protein - useful
 PT for modulating programmed cell death
 XX XX
 PS Disclosure; Columns 13-16; 26pp; English.
 XX XX
 CC The present sequence encodes rat bcl-2 protein (Rbcl-2). The
 CC specification also describes human bcl-2 protein (Hbcl-2). Rbcl-2 and
 CC Hbcl-2 are homologues of the bcl-2 protein thought to be involved in
 CC programmed cell death (apoptosis and necrosis). Rbcl-2 and Hbcl-2
 CC proteins may be used to treat conditions associated with a disruption of
 CC the cell death pathway. If they act as cell death inhibitors, they may be
 CC used in therapies to treat subjects suffering from: strokes, head trauma,
 CC Alzheimer's disease, neural and muscular degenerative diseases
 CC (especially multiple sclerosis), myocardial infarction, vitally induced
 CC cell death, aging, spinal cord injuries and amyotrophic lateral
 CC sclerosis- conditions where cells under go premature cell death as a
 CC result of triggers which may or may not be apparent. They may also be
 CC used in this way to develop cell lines which remain viable in culture for
 CC an extended period. In contrast, if they act as cell death stimulators,
 CC Rbcl-2 and Hbcl-2 may be used to treat conditions associated with
 CC prolonged cell life span such as cancer (especially Kaposi's sarcoma and
 CC lung cancer) and auto/hyperimmune diseases. They may also be used to
 CC cause cell death in, and hence control, parasites.
 XX XX
 SQ Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 other;

Query Match 90.5%; Score 527.8; DB 20; Length 579;
 Best Local Similarity 94.5%; Pred. No. 9.6e-122;
 Matches 547; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 1 atgtgagaccagctgcgcccagacacagggctgtgtgcaagcttgaagttat 60
 Db 1 atgtgagaccagctgcgcccagacacagggctgtgtgcaagcttgaagttat 60
 Qy 61 aagctgagcagaggggtttgtctgtgagctggtcccgaggagggccacagagcttgc 120
 Db 61 aagctgagcagaggggtttgtctgtgagctggtcccgaggagggccacagagcttgc 120
 Qy 121 ccgctgcacacagcattcgaggagctgagatgagttcagagccgcttcggcgccac 180
 Db 121 ccgctgcacacagcattcgaggagctgagatgagttcagagccgcttcggcgccac 180

Db 121 ccgctgcacacagcattcgaggagctgagatgagttcagagccgcttcggcgccac 180
 Qy 181 ttcttcgacatcgagcgtacgtacatgtgacccaggtcagccagcagcttcac 240
 Db 181 ttcttcgacatcgagcgtacgtacatgtgacccaggtcagccagcagcttcac 240
 Qy 241 caagtcaccagacattttcaaggaggcccaacttgaggccgcttgaagcttc 300
 Db 241 caagtcaccagacattttcaaggaggcccaacttgaggccgcttgaagcttc 300
 Qy 301 gctcttgaggctgcacatgtgtgtgagatgttcaacaagagatcagacacgtg 360
 Db 301 gctcttgaggctgcacatgtgtgtgagatgttcaacaagagatcagacacgtg 360
 Qy 361 caagtcagagatgtgagatgtgagatgtgagatgtgagatgtgagatgtgag 420
 Db 361 caagtcagagatgtgagatgtgagatgtgagatgtgagatgtgagatgtgag 420
 Qy 421 agtggggctgagcggagttcacagctctatacaggagagggccctgagagcg 480
 Db 421 agtggggctgagcggagttcacagctctatacaggagagggccctgagagcg 480
 Qy 481 cgtcgcggagggggaactgggacatcagtgagagacagtgctgagggcggtgac 540
 Db 481 cgtcgcggagggggaactgggacatcagtgagagacagtgctgagggcggtgac 540
 Qy 541 ggggcccgtgtaactcagagggcccttcttcagcaag 579
 Db 541 ggggcccgtgtaactcagagggcccttcttcagcaag 579

RESULT 8
 AAX25133
 ID AAX25133 standard; DNA; 581 BP.
 XX XX
 AC AAX25133;
 XX XX
 DT 05-JUL-1999 (first entry)
 XX XX
 DE Mouse bcl-2 gene.
 XX XX
 KW Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
 KW animal model; ss.
 XX XX
 OS Mus sp.
 XX XX
 PN W09913710-A1.
 XX XX
 PD 25-MAR-1999.
 XX XX
 PF 16-SEP-1998; 98WO-AU00764.
 XX XX
 PR 16-SEP-1997; 97AU-0009228.
 XX XX
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 XX XX
 PI Adams J, Cory S, Gibson L, Koenigen F, Print C;
 XX XX
 DR WPI; 1999-243890/20.
 XX XX
 PR P-PSDB; AAY05531.
 XX XX
 PT An animal model exhibiting reduced levels of a Bcl-2 protein and/or
 PT protein associated with Bcl-2
 XX XX
 PS Claim 3; Page 34; 52pp; English.

The present sequence is the mouse bcl-2 gene encoding Bcl-2 protein
 (see AAY05531), a pro-survival member of the Bcl-2 family which is
 widely expressed and which is essential for spermatogenesis. The
 invention relates generally to a method for treatment and to an
 animal model for the identification of molecules and genetic
 sequences useful for inducing or reducing fertility of male
 animals. Methods are provided for the treatment of infertility, or

XX Sequence 581 BP; 106 A; 158 C; 200 G; 117 T; 0 other;
SQ

[illegible]

QY

121 ccgctgcaccaagccatgtcggcgactgtgagatgaatttcgagaccgcttcccaggaa
|||||
|||tatccggcctctcatgagaacgatcttgagaccgcgtttccgcgcacc 180

[illegible][illegible][illegible][illegible]

Db 301 gtcttggggtgctgcctgtgtgctgagatgtcaacaagaatcgtgagcctcttcttcttga 42

[illegible]

421 agtggggtctggcggagttcaacgctctatcgggacggggcccttgagagagggcg 48

Dd 421 agtggggtctgcggagttcacagctctatacgggacggggcccccggaggagggcccc

[illegible]

541 ggagccctgtactgttagggcccttttgc tagcaagt 581
QY

Db 541 ggagccctgtactgtaggagcccttctgtcagcaagtcg 504

RESULT	9
AAT96578	

ID	standard; DNA; Sol. B.
XX	AAT96578
AC	AAT96578;

22-APR-1998 (first entry)

XX Mouse bcl-w DNA.
XX DE
XX bcl-2: cell survival; treatment; therapy; cancer

XX
KM
KM
diagnosis; degenerative disease; ss.
Bcl-w; apoptosis; cell
XX

OS
Mus sp.
XX

```
FT /product= bcl-w
FT /note= "q"
FT
```

PD	02-OCT-1997.	
XX		
DE	27-MAR-1997;	97WO-AU00199.

XX 96AU-0008965
PR 27-MAR-1996;

XX (AMRA-) AMRAD OPERATIONS PTY LTD.
PA
XX

PI Adams JM, Coly S, Green M
XX
DR WPI; 1997-489635/45.

DR p-PDSB; AAW36048.
XX Nucleic acid encoding apoptosis related gene bcl-2 - used to induce
PT treatment for cancer and

PT or inhibit cell survival
PT degenerative diseases

XX Claim 3; page 50-51; 86pp; English.
PS
XX

CC This sequence encodes the cell survival, so its modulation is used
CC family. This gene promotes diseases, degenerative diseases (e.g.
CC treatment of cancer or auto-immune diseases, degenerative degeneration,
CC treatment of cancer or auto-immune diseases, degenerative degeneration,
CC treatment of cancer or auto-immune diseases, degenerative degeneration,

stroke, Alzheimer's disease, myotonic dystrophy, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. up-regulation of the gene can also be used to modify cell transplants. up-regulation of the gene can also be used to modify cell transplants. up-regulation of the gene can also be used to modify cell transplants.

lines cultured in vivo, e.g., to develop "survival of primary explants" or to increase survival of hybridomas and to produce recombinant Bcl- κ -isolation of hybridomas. It can be used for screening of potential genetic modification.

CC during gene expression of secretory proteins.
CC for therapy, diagnosis, antibody production or screening.
CC modulators.

XX	Sequence	581 BP;	105 A;	164 C;	195 G;	117 T;	0 other;
SQ							

Query Match	Score 505.8; DB 18;	Length 581;
Best Local Similarity	Pred. No. 2.8e-116;	Indels 0; Gaps
	Matches 47;	

	Conservative	0;	Mismatches
Matches	534;			
1	atggcagacccctcgccccagacacacggtctgtgtgcagactttagttat	60		

[illegible][illegible]

Dc
61 agcgctgagcgagaagggttaccgcggccgcccgcgcaccc 180

Dd
121 ccacttcacccaagcatgctcgggcagcttgtagatgaacacccgcttcgcggcaccc 180

Db 121 ccgctgcaccaagcatgctggctgctgagacagagttgagaccggtttccgcgcgacc 180

QY

181 ttctcgtatctggcgagtcacgctgcattgatgaccaccaaggctccatgccaaagaaggaataaa
||||||| |||| | ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | |||||
tttccccctcacctcatcaactgaacctgacccagagtctagcccagcaacgcttcacc 240

Db 181 ttctctgacccgctccagccacacacg 300
 241 cagctctccgaacgaacttttaaggggccccaactggggcgcccttgtagcctcttt 300

241 caggttcgcgaactttccaaaggggccctaacttggggcgcgtcttgtgcatctctt 300

QY 301 gctctgggagcgtgcacigtgtgtccatgagagtgttcaacaagaagtcga
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
ttctttttttttcccccttatctgcctgagagtgtcaacaagaattgtagccttctgttgga 360

Dd	361	gccccgggggcgaacacgtccttcctccgagcgagcgcctgactgatacaaac	420
QY	361	caagtgcaggatgcgatggtgacctaccctgagaacgcgcctgactgatacaaac	420

Db 361 caagtcacagatctgatlctgacctactgtgagacacgctctgtgctgactggtgaltccatgac

QY 421 agtgggagctggcggaattcacagctctatacgggagcgggccctgagagagcgcg 480
 DB 421 agtggcgagctggcggaattcacagctctatacgggagcgggccctgagagagcgcg 480
 QY 481 gcttcgagggaggggaactgggcatcagtagagagagctctcagggggcgctggcaactg 540
 DB 481 gcttcgagggaggggaactgggcatcagtagagagagctctcagggggcgctggcaactg 540
 QY 541 ggggcccctgttaactgttaggggccccttttctgctagcaactg 581
 DB 541 ggggcccctgttaactgttaggggccccttttctgctagcaactg 581

RESULT 10

AAK25135
 ID AAK25135 standard; DNA; 581 BP.

AC AAK25135;

DT 05-JUL-1999 (first entry)

DE Mouse bcl-w gene derivative.

KW Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
 animal model; ss.

OS Mus sp.

Key Location/Qualifiers
 CDS 1..507
 /*tag= a

W09913710-A1.

25-MAR-1999.

16-SEP-1998; 98WO-AU00764.

16-SEP-1997; 97AU-0009228.

(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

Adams J, Cory S, Gibson L, Koentgen F, Print C;
 WPI: 1999-243890/20.

DR P-PSDB; AAY05533.

PS An animal model exhibiting reduced levels of a Bcl-w protein and/or
 protein associated with Bcl-w

Disclosure: Page 38; 52pp; English.

The present sequence is described as a derivative of the mouse
 bcl-w gene (see AAK25133) and encodes Bcl-w protein (see AAY05533), a
 pro-survival member of the Bcl-2 family which is widely expressed
 and which is essential for spermatogenesis. The invention relates
 generally to a method of treatment and to an animal model for the
 identification of molecules and genetic sequences useful for the
 inducing or reducing fertility of male animals. Methods are
 provided for the treatment of infertility, or for reducing
 fertility, by modulating spermatogenesis. An animal model carries
 a mutation in at least one allele of the human or murine bcl-w gene
 or in a gene associated with bcl-w. Such animals have disorganised
 seminiferous tubules and are substantially infertile, but possess no
 other major abnormalities as determined by histological examination.
 They can be used to screen for therapeutic molecules including
 genetic sequences capable of inducing, enhancing or otherwise
 facilitating spermatogenesis in animals, or which can induce
 infertility.

Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 other;

Query Match Best Local Similarity 86.8%; Score 505.8; DB 20; Length 581;
 Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 atggcgagcccgagcctcgcccgagacacacgagccttggtgacagcttgaggat 60
 DB 1 atggcgagcccgagcctcgcccgagacacacgagccttggtgacagcttgaggat 60
 QY 61 aagctgagcagagaggttattgtctgtgagctgctgcccgggagggcccaagcaactgac 120
 DB 61 aagctgagcagagaggttattgtctgtgagctgctgcccgggagggcccaagcaactgac 120
 QY 121 ccgctgacccaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
 DB 121 ccgctgacccaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
 QY 181 ttcttgatctggcgagctgagctgagctgagctgagctgagctgagctgagctgagctgagct 240
 DB 181 ttcttgatctggcgagctgagctgagctgagctgagctgagctgagctgagctgagctgagct 240
 QY 241 caagctcgcagagacttttcaaggggggcccaactgggcccgttgagcctctt 300
 DB 241 caagctcgcagagacttttcaaggggggcccaactgggcccgttgagcctctt 300
 QY 301 gctcttgagggctgagctgtgctgagagtgtaacaagagagatggaacacagctggga 360
 DB 301 gctcttgagggctgagctgtgctgagagtgtaacaagagagatggaacacagctggga 360
 QY 361 caagtcagagagtgatgtgtgctgagctgagcagcagcagcagcagcagcagcagcagc 420
 DB 361 caagtcagagagtgatgtgtgctgagctgagcagcagcagcagcagcagcagcagcagc 420
 QY 421 agtgggagctggcggaattcacagctctatacgggagcgggccctgagagagcgcg 480
 DB 421 agtgggagctggcggaattcacagctctatacgggagcgggccctgagagagcgcg 480
 QY 481 gcttcgagggaggggaactgggcatcagtagagagagctctcagggggcgctggcaactg 540
 DB 481 gcttcgagggaggggaactgggcatcagtagagagagctctcagggggcgctggcaactg 540
 QY 541 ggggcccctgttaactgttaggggccccttttctgctagcaactg 581
 DB 541 ggggcccctgttaactgttaggggccccttttctgctagcaactg 581

RESULT 11

AAV41925
 ID AAV41925 standard; cDNA; 1098 BP.

AC AAV41925;

DT 20-NOV-1998 (first entry)

DE Nucleotide sequence of the cDNA clone Bcl-1-like (HAICH29).

KW Bcl-1-like (HAICH29); chronic inflammatory disease; allergic reaction;
 immunological disorder; autoimmune disease; anti-infectious agent; ss.

OS Homo sapiens.

Key Location/Qualifiers
 CDS 1..1098
 /*tag= a
 /product= "Bcl-1-like (HAICH29) protein"

W09831800-A2.

23-JUL-1998.

21-JAN-1998; 98WO-US00960.

21-JAN-1997; 97US-0034205.

PR 21-JAN-1997; 97US-0034204.
 XX
 XX (AUCK-) AUCKLAND UNISERVICES LTD.
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX Feng P, Gentz RL, Krissansen GW, NI J, Rosen CA:
 PI Su JY;
 XX WPI; 1998-41409/35.
 DR P-PSDB; AAW59884.
 XX
 XX New isolated polynucleotides and encoded polypeptides - used to
 PT develop products for treating e.g. inflammatory diseases, allergies
 PT infections, immunological disorders, autoimmune diseases, or tumours
 PT or tumours
 PS Claim 2; Fig 12A-12D; 120pp; English.
 XX
 XX This is the nucleotide sequence of the cDNA clone Bcl-like (HAICH29),
 CC used in the method of the invention. The products of the clone can be
 CC used for treating conditions associated with abnormal expression of
 CC the polypeptides. They can be used for e.g. treating chronic
 CC inflammatory diseases, immunological disorders, autoimmune diseases,
 CC inflammatory diseases, various allergies, and as anti-infectious agents.
 CC The products can also be used for detection and diagnosis.
 CC
 XX Sequence 1098 BP; 264 A; 279 C; 325 G; 230 T; 0 other:

Query Match 73.6%; Score 428.8; DB 19; Length 1098;
 Best Local Similarity 99.5%; Pred. No. 4; 2e-97;
 Matches 430; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 atggcagcccccagctcgcccccagacacagcggctctgtgacagacttgaagtat 60
 1 atggcagcccccagctcgcccccagacacagcggctctgtgacagacttgaagtat 60
 DB 1 atggcagcccccagctcgcccccagacacagcggctctgtgacagacttgaagtat 60
 OY 61 aagctcagcagcagaggtatgtctgtgagctgccccggggagggccagcagctgac 120
 61 aagctcagcagcagaggtatgtctgtgagctgccccggggagggccagcagctgac 120
 DB 61 aagctcagcagcagaggtatgtctgtgagctgccccggggagggccagcagctgac 120
 OY 121 ccgctgacacacagcagctgagcagctgagatgagtcgagaccgcttcgcgcac 180
 121 ccgctgacacacagcagctgagcagctgagatgagtcgagaccgcttcgcgcac 180
 DB 121 ccgctgacacacagcagctgagcagctgagatgagtcgagaccgcttcgcgcac 180
 OY 181 ttctctatctgagcagctcagctgcatgtgacccagcgtcagcccaacagcttaac 240
 181 ttctctatctgagcagctcagctgcatgtgacccagcgtcagcccaacagcttaac 240
 DB 181 ttctctatctgagcagctcagctgcatgtgacccagcgtcagcccaacagcttaac 240
 OY 241 caggtctcgaagacttttcaaggggcccaactgaggcgccgttgaactctt 300
 241 caggtctcgaagacttttcaaggggcccaactgaggcgccgttgaactctt 300
 DB 241 caggtctcgaagacttttcaaggggcccaactgaggcgccgttgaactctt 300
 OY 301 gctcttgagcagctgctgtgctgagatgtcaacaagagatggaacactgtgga 360
 301 gctcttgagcagctgctgtgctgagatgtcaacaagagatggaacactgtgga 360
 DB 301 gctcttgagcagctgctgtgctgagatgtcaacaagagatggaacactgtgga 360
 OY 361 caagtgcagagtgagatgctgctacactgagacgagcgtgctgactgataccagc 420
 361 caagtgcagagtgagatgctgctacactgagacgagcgtgctgactgataccagc 420
 DB 361 caagtgcagagtgagatgctgctacactgagacgagcgtgctgactgataccagc 420
 OY 421 agtgggggctgg 432
 421 agtgggggctgg 432
 DB 421 agtgggggctgg 432

RESULT 12
 AAV59630
 ID AAV59630 standard; DNA; 1864 BP.
 XX
 AC AAV59630;
 XX
 DT 19-JAN-1999 (first entry)

XX
 XX Human secreted protein gene 120 clone HGB6764.
 KW Human: secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX
 OS Homo sapiens.
 XX
 XX W09839448-A2.
 XX
 PD 11-SEP-1998.
 XX
 XX 06-MAR-1998; 98WO-0504493.
 PF
 XX
 XX 02-OCT-1997; 97US-0061060.
 PR 07-MAR-1997; 97US-0038621.
 PR 07-MAR-1997; 97US-0040161.
 PR 07-MAR-1997; 97US-0040162.
 PR 07-MAR-1997; 97US-0040163.
 PR 07-MAR-1997; 97US-0040334.
 PR 07-MAR-1997; 97US-0040336.
 PR 07-MAR-1997; 97US-0040626.
 PR 11-APR-1997; 97US-0043311.
 PR 11-APR-1997; 97US-0043312.
 PR 11-APR-1997; 97US-0043313.
 PR 11-APR-1997; 97US-0043314.
 PR 11-APR-1997; 97US-0043568.
 PR 11-APR-1997; 97US-0043569.
 PR 11-APR-1997; 97US-0043570.
 PR 11-APR-1997; 97US-0043571.
 PR 11-APR-1997; 97US-0043572.
 PR 11-APR-1997; 97US-0043574.
 PR 11-APR-1997; 97US-0043576.
 PR 11-APR-1997; 97US-0043578.
 PR 11-APR-1997; 97US-0043580.
 PR 11-APR-1997; 97US-0043581.
 PR 11-APR-1997; 97US-0043582.
 PR 11-APR-1997; 97US-0043583.
 PR 11-APR-1997; 97US-0043584.
 PR 11-APR-1997; 97US-0043585.
 PR 11-APR-1997; 97US-0043586.
 PR 11-APR-1997; 97US-0043587.
 PR 11-APR-1997; 97US-0043588.
 PR 11-APR-1997; 97US-0043589.
 PR 11-APR-1997; 97US-0043590.
 PR 11-APR-1997; 97US-0043591.
 PR 11-APR-1997; 97US-0043592.
 PR 11-APR-1997; 97US-0043593.
 PR 11-APR-1997; 97US-0043594.
 PR 11-APR-1997; 97US-0043595.
 PR 11-APR-1997; 97US-0043596.
 PR 11-APR-1997; 97US-0043597.
 PR 11-APR-1997; 97US-0043598.
 PR 11-APR-1997; 97US-0043599.
 PR 11-APR-1997; 97US-0043600.
 PR 11-APR-1997; 97US-0043601.
 PR 11-APR-1997; 97US-0043612.
 PR 11-APR-1997; 97US-0043613.
 PR 11-APR-1997; 97US-0043614.
 PR 11-APR-1997; 97US-0043615.
 PR 11-APR-1997; 97US-0043616.
 PR 11-APR-1997; 97US-0043617.

Query Match	Best Local Similarity	Score	DB	Length
Matches 429; Conservative 1; Mismatches 2; Indels 0; Gaps 0	99.3%;	428.4;	DB 19;	1864;
QY 1 atgagcagcccccagcctccgccccagacacagcggctctgtgcagacattgtatgtat 60				
DB 11 atgagcagcccccagcctccgccccagacacagcggctctgtgcagacattgtatgtat 70				
QY 61 aagctagcagcagaaggttatgtctgtgaaagctgcccccgaggagccagacagtac 120				
DB 71 aagcctgagcagcagaaggttatgtctgtgaaagctgcccccgaggagccagacagtac 130				
QY 121 ccgcttcacacaaagccatgcggcagcagctgagatgagttcgtgagaccgcgttcggcgacc 180				
DB 131 ccgcttcacacaaagccatgcggcagcagctgagatgagttcgtgagaccgcgttcggcgacc 190				
QY 181 tctctctgactctgagcgtctcagctgcacatgtacccagcgtccagccagacagcttcacc 240				
DB 191 tctctctgactctgagcgtctcagctgcacatgtacccagcgtccagccagacagcttcacc 250				
QY 241 cagagctctcagcagacattttcaaggaggggccccaacttgggcccgccttgtagcctctt 300				
DB 251 cagagctctcagcagacattttcaaggaggggccccaacttgggcccgccttgtagcctctt 310				
QY 301 gtctttggggctgtcactgtgtctgaaagtgtaacaagaagatagaaacacactgtgga 360				
DB 311 gtctttggggctgtcactgtgtctgaaagtgtaacaagaagatagaaacacactgtgga 370				
QY 361 caagctgacagagatgagatgtgtgacctcctggagacagcggtctgactgtagtcacagc 420				
DB 371 caagctgacagagatgagatgtgtgacctcctggagacagcggtctgactgtagtcacagc 430				
QY 421 agtggggggctgg 432				
DB 431 agtggggggctgg 442				

Sequence 1864 BP; 494 A; 403 C; 506 G; 455 T; 6 other;

Query Match: 73.5%; Score 428.4; DB 19; Length 1864; Best Local Similarity 99.3%; Pred. No. 6e-97; Mismatches 2; Indels 0; Gaps 0

Matches 429; Conservative 1; Mismatches 2; Indels 0; Gaps 0

QY 1 atgagcagcccccagcctccgccccagacacagcggctctgtgcagacattgtatgtat 60

DB 11 atgagcagcccccagcctccgccccagacacagcggctctgtgcagacattgtatgtat 70

QY 61 aagctagcagcagaaggttatgtctgtgaaagctgcccccgaggagccagacagtac 120

DB 71 aagcctgagcagcagaaggttatgtctgtgaaagctgcccccgaggagccagacagtac 130

QY 121 ccgcttcacacaaagccatgcggcagcagctgagatgagttcgtgagaccgcgttcggcgacc 180

DB 131 ccgcttcacacaaagccatgcggcagcagctgagatgagttcgtgagaccgcgttcggcgacc 190

QY 181 tctctctgactctgagcgtctcagctgcacatgtacccagcgtccagccagacagcttcacc 240

DB 191 tctctctgactctgagcgtctcagctgcacatgtacccagcgtccagccagacagcttcacc 250

QY 241 cagagctctcagcagacattttcaaggaggggccccaacttgggcccgccttgtagcctctt 300

DB 251 cagagctctcagcagacattttcaaggaggggccccaacttgggcccgccttgtagcctctt 310

QY 301 gtctttggggctgtcactgtgtctgaaagtgtaacaagaagatagaaacacactgtgga 360

DB 311 gtctttggggctgtcactgtgtctgaaagtgtaacaagaagatagaaacacactgtgga 370

QY 361 caagctgacagagatgagatgtgtgacctcctggagacagcggtctgactgtagtcacagc 420

DB 371 caagctgacagagatgagatgtgtgacctcctggagacagcggtctgactgtagtcacagc 430

QY 421 agtggggggctgg 432

DB 431 agtggggggctgg 442

RESULT 13

ABL32228

ID ABL32228 standard; DNA: 6049 BP.

XX

AC ABL32228;

XX

DT 26-MAR-2002 (first entry)

XX

DE Human immune system associated gene SEQ ID NO: 201.

XX

Human: immune system disease; cytosine methylation; antiasthmatic; antilarteriosclerotic; antianaemic; cytosolic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene; ds.

XX

OS Homo sapiens.

XX

PN W0200200928-A2.

XX

03-JAN-2002.

XX

PD 02-JUL-2001; 2001WO-EP07537.

XX

PF

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 6, 2002, 12:02:24 ; Search time 295.22 Seconds
(without alignments)
3384.744 Million cell updates/sec

Title: US-09-155-327E-8

Perfect score: 582
Sequence: 1 atggcgacccccgcctcaac.....ccttttgcctagaagta 582

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N.Geneseq-032802:*

1: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
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5: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
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21: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	577.8	99.3	581	20	AAV25133
2	563.4	96.8	581	18	AAV25133
3	563.4	96.8	581	20	AAV25133
4	558.2	95.9	579	19	AAV25133
5	558.2	95.9	579	20	AAV25133
6	520.2	89.4	581	20	AAV25133
7	519.6	89.3	583	18	AAV25133
8	519.6	89.3	583	20	AAV25133
9	515	88.3	579	19	AAV25133

10	515	88.5	579	20	AAV15946
11	372.8	64.1	1098	19	AAV41925
12	372.4	64.0	1864	19	AAV59630
13	218.6	37.6	6049	24	ABL32228
14	192.6	33.1	6049	24	ABL32229
15	148.4	25.5	150	22	ABA47382
16	148.4	25.5	150	22	ABA65269
17	148.4	25.5	150	22	ABA32370
18	148.4	25.5	150	22	AAK13683
19	148.4	25.5	150	22	AAK39424
20	148.4	25.5	150	22	AAI20236
21	148.4	25.5	150	22	AAI45438
22	148.4	25.5	150	22	AAI05940
23	135	23.2	1742	22	AAV75960
24	134.6	23.1	636	22	AAH48169
25	134.6	23.1	702	22	AAH43464
26	134.6	23.1	926	16	AAO81698
27	134.6	23.1	926	17	AAV40079
28	134.6	23.1	926	21	AAV29614
29	134.6	23.1	926	21	AAV15189
30	134.6	23.1	926	22	AAV090810
31	134.6	23.1	1236	22	AAV00247
32	134.6	23.1	1455	22	AAV33182
33	131.2	22.5	1455	22	AAV00250
34	129.6	22.3	747	22	AAV30926
35	126.8	21.8	600	22	ABA60917
36	126.8	21.8	600	22	ABA28894
37	126.8	21.8	600	22	AAK09207
38	126.8	21.8	600	22	AAK35096
39	126.8	21.8	600	22	AAI40812
40	126.8	21.8	720	22	AAH45295
41	125.8	21.6	555	22	AAV73433
42	125.8	21.6	555	22	ABA38761
43	125.8	21.6	555	22	AAK21876
44	125.8	21.6	555	22	AAK48039
45	125.8	21.6	555	22	AAV53868

ALIGNMENTS

RESULT 1	
AAV25133	standard; DNA: 581 BP.
ID	AAV25133
XX	AAV25133;
AC	05-JUL-1999 (first entry)
XX	
DE	Mouse bcl-w gene.
XX	
KW	Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
KW	animal model; ss.
XX	
OS	Mus sp.
XX	
PN	WO9913710-A1.
XX	
PD	25-MAR-1999.
XX	
PF	16-SEP-1998; 98WO-AU00764.
XX	
PR	16-SEP-1997; 97AU-0009228.
XX	
PA	(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX	
PI	Adams J, Cory S, Gibson L, Koenigen F, Print C;
XX	WPL; 1999-243890/20.
DR	P-PSDB; AAV05531.
XX	
PT	An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w

CDNA encoding the Nucleotide sequence Human secreted pro Human immune syste Human breast cell Human foetal liver Probe #10836 for g Human brain expres Human bone marrow Probe #10169 for g Probe #14124 used t Probe #5931 used t Rat wild-type Bcl- Mutant bcl-XL codi CDNA clone HP03564 Human thymus Bcl-X Bcl-XL gene. Homo Bcl-X gene. Homo Human bcl-x cdna. Human Bcl-XL nucle Bcl-XL-DTR apoptos Base sequence of t Lfh-Bcl-XL apoptos Human Bcl-XL (tran Human foetal liver Probe #7360 for ge Human brain expres Human bone marrow Probe #9498 used t DNA encoding human Human foetal liver Probe #17227 for g Human brain expres Human bone marrow Probe #22554 used

XX Claim 3; Page 34; 52pp; English
PS
XY

CC The present sequence is the mouse bcl-w gene encoding Bcl-w protein
CC (see AAY05311), a pro-survival member of the Bcl-2 family which is
CC widely expressed and which is essential for spermatogenesis. The
CC invention relates generally to a method of treatment and to an
CC animal model for the identification of molecules and genetic
CC sequences useful for inducing or reducing fertility of male
CC animals. Methods are provided for the treatment of infertility, or
CC for reducing fertility, by modulating spermatogenesis. An animal
CC model carries a mutation is at least one allele of the human or
CC murine bcl-w gene or in a gene associated with bcl-w. Such animals
CC have disorganised seminiferous tubules and are substantially
CC infertile, but possess no other major abnormalities as determined
CC by histological examination. They can be used to screen for
CC therapeutic molecules including genetic sequences capable of
CC inducing, enhancing or otherwise facilitating spermatogenesis in
CC animals, or which can induce infertility.

50 Sequence 581 BP; 106 A; 158 C; 200 G; 117 T; 0 other;

Query Match	99.38;	Score 577.8;	DB 20;	Length 581;
Best Local Similarity	99.78;	Pred. No. 3.4e-145;		
Matches 579;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0

QY	1	atgacgagcccaacccccaacccccaacaaacagggctctatgtgctactctttatgagctat	6
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QY	61	agagctgagcgagaaaggatgatgtctgtgagctctgccccttggggaagagccacgcgcgac	121
Db	61	aagctgagagcgagaaaggatgatgtctgtgagctctgccccttggggaagagccacgcgcgac	121
QY	121	ccgctgcacacaaagccatgagggtctgtctgtgaaagcaagttctagaaccggtttccgcgcgac	181
Db	121	ccgctgcacacaaagccatgagggtctgtctgtgaaagcaagttctagaaccggtttccgcgcgac	181
QY	181	ttctctgaccttgccagctcagctacgctgagccccaagcccaacgaacagcttcaac	241
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QY	241	caggttccgacgaacattttccaagaggggcccttaacgcggtctctgtgcatcttt	301
Db	241	caggttccgacgaacattttccaagaggggcccttaacgcggtctctgtgcatcttt	301
QY	301	gtctttgggggtcgccctctgtgtctgtgagaggttcaacaaagaatgtgagcctttgtgtgga	361
Db	301	gtctttgggggtcgccctctgtgtctgtgagaggttcaacaaagaatgtgagcctttgtgtgga	361
QY	361	caagctgcagagatgtgagctgtgagcccttgaagagacagctctgtgctatcaggtttccacagc	421
Db	361	caagctgcagagatgtgagctgtgagcccttgaagagacagctctgtgctatcaggtttccacagc	421
QY	421	agtgcgagctgtgagcgaggtttcaacagctctatacggggaacgggccccttgagagagcgag	481
Db	421	agtgcgagctgtgagcgaggtttcaacagctctatacggggaacgggccccttgagagagcgag	481
QY	481	cgctctgcggagaggggaactgtgagcatcagttgagacagtgctgacgggggcgtgtgacctg	541
Db	481	cgctctgcggagaggggaactgtgagcatcagttgagacagtgctgacgggggcgtgtgacctg	541
QY	541	ggggcccttgtaactgtaggggacctttttgtctagcaagtg	581
Db	541	ggggcccttgtaactgtaggggacctttttgtctagcaagtg	581

RESULT	2
AAT96578	
ID	AAT96578 standard; DNA; 581 BP
XX	
AC	AAT96578;

XX	22-APR-1998	(first entry)
DT		
XX		

KM Bcl-2; apoptosis; bcl-2; cell survival; treatment; therapy; cancer
KW diagnosis; degenerative disease; ss.
XY

FH	Key	Location/Qualifiers
FT	CDS	1..507
FM		/*tag 3

PN W09735971-A1
XY

PD 02-OCT-1997
XX

PE 27-MAR-1997; 97WO-A000199;
XX

PK	2/-MAR-1996;	96AD-0008965.
XX		

PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX

Pl Adams JM, Cory S, Gibson LM, Holmgreen SP;
XX

DR WPL: 199/-489635/45.
DR P-PSDB: AAW36048

XX	Nucleic acid enc
PT	

PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce
PT or inhibit cell survival, e.g. for treatment of cancer and
PT degenerative diseases

PS Claim 3; Page 50-51; 86pp; English.

CC This sequence encodes a novel gene, bcl-1w, from the mouse bcl-2 gene
CC family. This gene promotes cell survival, so its modulation is useful in
CC treatment of cancer or auto-immune diseases, degenerative diseases (e.g.
CC stroke, Alzheimer's disease, myocardial infarct, muscular degeneration,
CC hypoxia, ischaemia, human immunodeficiency virus infection or in cell
CC transplants. Up-regulation of the gene can also be used to modify cell
CC lines cultured in vivo, e.g. to develop new lines, to facilitate
CC isolation of hybridomas and to increase survival of primary explants
CC during genetic modification. It can be used to produce recombinant Bcl-1w
CC for therapy, diagnosis, antibody production or screening of potential
CC modulators.

SQ Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 other;

Query Match	96.8%;	Score 563.4;	DB 18;	Length 581;
Best Local Similarity	98.1%;	Pred. No. 2.5e-141;		
Matches 570;	Conservative	0;	Mismatches 11;	Indels 0;
				Gaps 0;

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	111		
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QY	61	aggtctgagagcagaaagaggttactgtctctgtgagatctgagccctgtggagaaagccacgcgcgcgac	120
	61	aggtctgagagcagaaagaggttactgtctctgtgagatctgagccctgtggagaaagccacgcgcgcgac	120
Db	61	aggtctgagagcagaaagaggttactgtctctgtgagatctgagccctgtggagaaagccacgcgcgcgac	120
QY	121	cgcgtctgacacaaagaccatgacgagcgtctgctcgtcgagagagaaatttgaaacccgtttccgcgcgcac	180
	121		
Db	121	cgcgtctgacacaaagaccatgacgagcgtctgctcgtcgagagagaaatttgaaacccgtttccgcgcgcac	180
QY	181	tctctctgacactctgcgcgtctcacaactacacgttbaaccccgaggtctcagccacgaacagctctaac	240
	181		
Db	181	tctctctgacactctgcgcgtctcacaactacacgttbaaccccgaggtctcagccacgaacagctctaac	240
QY	241	caaggtttccgcgacgaactttttccaaagggggcctcaactctgaggtgcgcgtctgtgtgacatctctt	300


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|||||
Db 241 caggttccgcagcaactttccaaggggccctactgaggccgtctctgacatctt 300
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OY 301 gtcttggggtccctgtgtgctgagagttcaacaagaatgagccttctgtgga 360
Db 301 gtcttggggtccctgtgtgctgagagttcaacaagaatgagccttctgtgga 360
OY 361 caagtgcagatgtgatgtgtgctactgagacacgtctgtgctgactgatacagc 420
Db 361 caagtgcagatgtgatgtgtgctactgagacacgtctgtgctgactgatacagc 420
OY 421 agtgcggtctggcgaggtacacactctatacggggagccctggagagcgacgg 480
OY 421 agtgcggtctggcgaggtacacactctatacggggagccctggagagcgacgg 480
Db 421 agtgcggtctggcgaggtacacactctatacggggagccctggagagcgacgg 480
OY 481 cgtctgcggagggaggaactgggcatcagtgagagacagtcgtacggggcggtgcactg 540
Db 481 cgtctgcggagggaggaactgggcatcagtgagagacagtcgtacggggcggtgcactg 540
OY 541 ggggccctgttaactgtaggggccttttctgtaagaagt 581
Db 541 ggggccctgttaactgtaggggccttttctgtaagaagt 581

RESULT 3
AAK25135
ID AAK25135 standard; DNA; 581 BP.
XX
AC AAK25135;
XX
XX 05-JUL-1999 (first entry)
DE Mouse bcl-w gene derivative.
XX
XX Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
KW animal model; ss.
XX
OS Mus sp.
XX
XX Key Location/Qualifiers
FH 1..507
FT CDS /*tag= a
PI
XX WO9913710-A1.
XX
XX 25-MAR-1999.
XX
XX 16-SEP-1998; 98WO-AU00764.
XX
XX 16-SEP-1997; 97AU-0009228.
XX
XX (HALT-) HALT INST MEDICAL RES WALTER & ELIZA.
XX
XX Adams J, Cory S, Gibson L, Koentgen F, Print C;
XX
XX MPI, 1999-243890/20.
XX
XX P-PSDB; AA105533.
XX
XX An animal model exhibiting reduced levels of a Bcl-w protein and/or
XX protein associated with Bcl-w
XX
XX Disclosure; Page 38; 52pp; English.
XX
XX The present sequence is described as a derivative of the mouse
XX bcl-w gene (see AAK25133) and encodes Bcl-w protein (see AA105533), a
XX pro-survival member of the Bcl-2 family which is widely expressed
XX and which is essential for spermatogenesis. The invention relates
XX generally to a method of treatment and to an animal model for the
XX identification of molecules and genetic sequences useful for
XX inducing or reducing fertility of male animals. Methods are
XX provided for the treatment of infertility, or for reducing
XX fertility, by modulating spermatogenesis. An animal model carries
XX a mutation is at least one allele of the human or murine bcl-w gene

```

or in a gene associated with bcl-w. Such animals have disorganised seminiferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility.

Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 other;

Query Match 96.8%; Score 563.4; DB 20; Length 581;
Best Local Similarity 98.1%; Pred. No. 2.5e-141;
Matches 570; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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OY 1 atggcgaccccgctcaccacacacagcggtcctcagtggtgctgtgtagctat 60
Db 1 atggcgaccccgctcaccacacacagcggtcctcagtggtgctgtgtagctat 60
OY 61 aggtcagcagagaaggtatgtctgtgagctgtggtcctggggaagccagccgagac 120
Db 61 aggtcagcagagaaggtatgtctgtgagctgtggtcctggggaagccagccgagac 120
OY 121 ccgctgcacacacacacacacacacacacacacacacacacacacacacacacac 180
Db 121 ccgctgcacacacacacacacacacacacacacacacacacacacacacacacac 180
OY 181 ttctctgacctgtgcgctcagctacacgtagccacagccagccagccagccagccac 240
Db 181 ttctctgacctgtgcgctcagctacacgtagccacagccagccagccagccagccac 240
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Db 241 caaggttcgcagcaactttccaagggggcccctaactgggcccgtcttctgtgcatctt 300
OY 301 gtcttggggtccctgtgtgctgagagtgtaacaagaatgagccttctgtgga 360
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OY 361 caagtgcagatgtgatgtgtgctactgagacacagtcgtgctgactgatacagc 420
Db 361 caagtgcagatgtgatgtgtgctactgagacacagtcgtgctgactgatacagc 420
OY 421 agtgcggtctggcgaggtacacactctatacggggagccctggagagcgacgg 480
Db 421 agtgcggtctggcgaggtacacactctatacggggagccctggagagcgacgg 480
OY 481 cgtctgcggagggaggaactgggcatcagtgagagacagtcgtacggggcggtgcactg 540
Db 481 cgtctgcggagggaggaactgggcatcagtgagagacagtcgtacggggcggtgcactg 540
OY 541 ggggccctgttaactgtaggggccttttctgtaagaagt 581
Db 541 ggggccctgttaactgtaggggccttttctgtaagaagt 581

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RESULT 4
AAV28333
ID AAV28333 standard; cDNA; 579 BP.
XX
XX AAV28333;
XX
XX 02-OCT-1998 (first entry)
XX
XX Rat bcl-y gene.
XX
XX ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
XX
XX Rattus sp.
XX
XX Key Location/Qualifiers
FH 1..579
FT CDS /*tag= a

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Query Match 95.9%: Score 558.2; DB 20; Length 579;
 Best Local Similarity 97.8%; Pred. No. 6,1e-140;
 Matches 566; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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DB 1 atggagaccacccagctcaacccacagacacagcggtctagtgtgcttgaagctat 60
QY 61 aggtgagcagaaaggttattgtctgtgagctgcccctggggaagccagcccgac 120
   |||||
DB 61 aggtgagcagaaaggttattgtctgtgagctgcccctggggaagccagcccgac 120
QY 121 ccgctcaccacaaagcagctgagcgctgtggaagagattgagaccgtttccgcccagc 180
   |||||
DB 121 ccgctcaccacaaagcagctgagcgctgtggaagagattgagaccgtttccgcccagc 180
QY 181 ttctctgacctgagcagctcagctacagctgagccaggtccagccacagcttcacc 240
   |||||
DB 181 ttctctgacctgagcagctcagctacagctgagccaggtccagccacagcttcacc 240
QY 241 caagttccagcaactttccaaaggggccctaactggggcgctctgtgcatctt 300
   |||||
DB 241 caagttccagcaactttccaaaggggccctaactggggcgctctgtgcatctt 300
QY 301 gctctggggcgctcctgtgtgtgtgagagtgatcaacaagaatgagccttggtgga 360
   |||||
DB 301 gctctggggcgctcctgtgtgtgtgagagtgatcaacaagaatgagccttggtgga 360
QY 361 caaattgacagatgagctgagctcagctcagctcagctcagctcagctcagctcagc 420
   |||||
DB 361 caaattgacagatgagctgagctcagctcagctcagctcagctcagctcagctcagc 420
QY 421 agtggcggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 480
   |||||
DB 421 agtggcggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 480
QY 481 cgtctgagcagagagagagagagagagagagagagagagagagagagagagagagag 540
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DB 481 cgtctgagcagagagagagagagagagagagagagagagagagagagagagagagag 540
QY 541 ggggcccgtgtaactgtaggggccccttttctgtagcaag 579
DB 541 ggggcccgtgtaactgtaggggccccttttctgtagcaag 579

```

RESULT 6
 AAX25132
 ID AAX25132 standard; DNA; 581 BP.

```

XX AAX25132:
AC 05-JUL-1999 (first entry)
DT 05-JUL-1999 (first entry)
XX Human bcl-w gene.
DE Human bcl-w gene.
XX Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
KW animal model; ss.
XX Homo sapiens.
OS Homo sapiens.
XX WO9913710-A1.
PN 25-MAR-1999.
XX 16-SEP-1998; 98MO-AU00764.
PF 16-SEP-1997; 97AU-0009228.
PR (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX PA
XX PI
XX Adams J, Cory S, Gibson L, Koentgen F, Print C;

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DR WPI: 1999-243890/20.
 DR P-PSDB: AAY05530.
 XX An animal model exhibiting reduced levels of a Bcl-w protein and/or
 PT protein associated with Bcl-w
 Claim 3; Page 32; 52pp; English.

The present sequence is the human bcl-w gene encoding Bcl-w protein (see AAY05530), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation in a gene associated with bcl-w. Such animals have disorganised seminiferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility.

Sequence 581 BP; 104 A; 155 C; 210 G; 112 T; 0 other;

Query Match 89.4%: Score 520.2; DB 20; Length 581;
 Best Local Similarity 93.5%; Pred. No. 9.2e-130;
 Matches 543; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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QY 1 atggagaccacccagctcaacccacagacacagcggtctagtgtgcttgaagctat 60
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DB 1 atggagaccacccagctcaacccacagacacagcggtctagtgtgcttgaagctat 60
QY 61 aggtgagcagaaaggttattgtctgtgagctgcccctggggaagccagcccgac 120
   |||||
DB 61 aggtgagcagaaaggttattgtctgtgagctgcccctggggaagccagcccgac 120
QY 121 ccgctcaccacaaagcagctgagcgctgtggaagagattgagaccgtttccgcccagc 180
   |||||
DB 121 ccgctcaccacaaagcagctgagcgctgtggaagagattgagaccgtttccgcccagc 180
QY 181 ttctctgacctgagcagctcagctacagctgagccaggtccagccacagcttcacc 240
   |||||
DB 181 ttctctgacctgagcagctcagctacagctgagccaggtccagccacagcttcacc 240
QY 241 caagttccagcaactttccaaaggggccctaactggggcgctctgtgcatctt 300
   |||||
DB 241 caagttccagcaactttccaaaggggccctaactggggcgctctgtgcatctt 300
QY 301 gctctggggcgctcctgtgtgtgtgagagtgatcaacaagaatgagccttggtgga 360
   |||||
DB 301 gctctggggcgctcctgtgtgtgtgagagtgatcaacaagaatgagccttggtgga 360
QY 361 caaattgacagatgagctgagctcagctcagctcagctcagctcagctcagctcagc 420
   |||||
DB 361 caaattgacagatgagctgagctcagctcagctcagctcagctcagctcagctcagc 420
QY 421 agtggcggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 480
   |||||
DB 421 agtggcggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 480
QY 481 cgtctgagcagagagagagagagagagagagagagagagagagagagagagagagag 540
   |||||
DB 481 cgtctgagcagagagagagagagagagagagagagagagagagagagagagagagag 540
QY 541 ggggcccgtgtaactgtaggggccccttttctgtagcaag 581
DB 541 ggggcccgtgtaactgtaggggccccttttctgtagcaag 581

```


or in a gene associated with bcl-2. Such animals have disorganised seminiferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility.

Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;

Query Match 89.3%; Score 519.6; DB 20; Length 583;
Best Local Similarity 93.3%; Pred. No. 1.3e-129;
Matches 543; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

1 atgagcaccacgactcaacccacacacgagctctagctgacttgaagctat 60
1 atgagcaccacgactcagccacacacgagctctgctgagcagacttgaagctat 60
61 agctgagcagagaggtatctgtgagctgagcctgaggaagccacgagcagc 120
61 agctgagcagagaggtatctgtgagctgagcctgaggaagccacgagcagc 120
121 ccgctgacacagacatgagctgctgagcagagtttgaagccgcttcgcagc 180
121 ccgctgacacagacatgagctgctgagcagagtttgaagccgcttcgcagc 180
181 tctctgacctgagcagctacagctgagcagcagcagcagcagcagcagc 240
181 tctctgacctgagcagctacagctgagcagcagcagcagcagcagcagc 240
241 caggttcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300
241 caggttcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300
301 gctcttgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 360
301 gctcttgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 360
361 caagtgcaagatgagctgagcagcagcagcagcagcagcagcagcagc 420
361 caagtgcaagatgagctgagcagcagcagcagcagcagcagcagcagc 420
421 agtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480
421 agtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480
481 cgtctgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 540
481 cgtctgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 540
541 ggggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 582
541 ggggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 582

RESULT 9
AAV28334
ID AAV28334 standard; cDNA; 579 BP.
XX AAV28334;
XX 02-OCT-1998 (first entry)
XX Human bcl-2 gene.
XX ss; bcl-2; cell death pathway; apoptotic; apoptosis; human.
XX Homo sapiens.
XX Key location/Qualifiers
XX 1, 579
XX CDS /tag- a
FT

/product= bcl-2
/note= "No stop codon given"

US5789201-A.

04-AUG-1998.

11-FEB-1997; 9705-0798897.

23-FEB-1996; 9605-0012201.

11-FEB-1997; 9705-0798897.

(COCE-) COCENSYS INC.

Guastella J;

WPI; 1998-446079/38.

P-PSDB; AAM61392.

Claim 3; Column 15/16; 27pp; English.

The mammalian bcl-2 genes encode a protein that is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activity and the apoptosis blocking activity. bcl-2 falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell death is desired.

Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;

Query Match 88.5%; Score 515; DB 19; Length 579;
Best Local Similarity 93.1%; Pred. No. 2.3e-128;
Matches 539; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

1 atgagcaccacgactcaacccacacacgagctctagctgacttgaagctat 60
1 atgagcaccacgactcagccacacacgagctctgctgagcagacttgaagctat 60
61 agctgagcagagaggtatctgtgagctgagcctgaggaagccacgagcagc 120
61 agctgagcagagaggtatctgtgagctgagcctgaggaagccacgagcagc 120
121 ccgctgacacagacatgagctgctgagcagagtttgaagccgcttcgcagc 180
121 ccgctgacacagacatgagctgctgagcagagtttgaagccgcttcgcagc 180
181 tctctgacctgagcagctacagctgagcagcagcagcagcagcagcagc 240
181 tctctgacctgagcagctacagctgagcagcagcagcagcagcagcagc 240
241 caggttcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300
241 caggttcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300
301 gctcttgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 360
301 gctcttgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 360
361 caagtgcaagatgagctgagcagcagcagcagcagcagcagcagcagc 420
361 caagtgcaagatgagctgagcagcagcagcagcagcagcagcagcagc 420
421 agtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480
421 agtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480

PR 21-JAN-1997: 97US-0034204.
XX (AUCK-) AUCKLAND UNISERVICES LTD.
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Feng P, Gentz RL, Krissansen GW, NI J, Rosen CA;
PI Su JY;
XX WPI, 1998-414099/35.
DR P-PSDB, AAM59884.
XX
PT New isolated polynucleotides and encoded polypeptides - used to
PT develop products for treating e.g. inflammatory diseases, allergies
PT infections, immunological disorders, autoimmune diseases, or tumours
PT or tumours
PS Claim 2; Fig 12A-12D; 120pp; English.
XX
XX This is the nucleotide sequence of the cDNA clone Bcl-11ke (HACH29),
CC used in the method of the invention. The products of the clone can be
CC used for treating conditions associated with abnormal expression of
CC the polypeptides. They can be used for e.g. treating chronic
CC inflammatory diseases, immunological disorders, autoimmune diseases,
CC inflammatory diseases, various allergies, and as anti-infectious agents.
CC The products can also be used for detection and diagnosis.
XX
XX Sequence 1098 BP; 264 A; 279 C; 325 G; 230 T; 0 other:

Query Match 64.1%; Score 372.8; DB 19; Length 1098;
Best Local Similarity 91.4%; Pred. No. 3.4e-90;
Matches 395; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 atggcgacccacgacgttaacccacagacacagcgctctgtggtcactttagatcat 60
DB 1 atggcgacccacgacgttaacccacagacacagcgctctgtggtcactttagatcat 60
QY 61 aggtcgagacgagaggttctgtctgtgagcctgcccctgggagagccacgacgac 120
DB 61 aggtcgagacgagaggttctgtctgtgagcctgcccctgggagagccacgacgac 120
QY 121 ccgctgcacacagcattgctgctgctgagcagcagtttagacccgcttcgacgac 180
DB 121 ccgctgcacacagcattgctgctgctgagcagcagtttagacccgcttcgacgac 180
QY 181 tctctgacgttgcgctcagctcagctcagctcagctcagctcagctcagctcagct 240
DB 181 tctctgacgttgcgctcagctcagctcagctcagctcagctcagctcagctcagct 240
QY 241 caggttccgacgacatttcccaaggagcccttaacttgggacgcttctgtgacatctt 300
DB 241 caggttccgacgacatttcccaaggagcccttaacttgggacgcttctgtgacatctt 300
QY 301 gttcttgggggctgctgtgtctgtagagtgcaacaagaatgagacgttctgtgga 360
DB 301 gttcttgggggctgctgtgtctgtagagtgcaacaagaatgagacgttctgtgga 360
QY 361 caagtcagagattgtagtgctcactcgtgagacacgttctgtgagacacgacgac 420
DB 361 caagtcagagattgtagtgctcactcgtgagacacgttctgtgagacacgacgac 420
QY 421 agtggcgagctgg 432
DB 421 agtggcgagctgg 432

RESULT 12
AAVS9630
ID AAVS9630 standard; DNA: 1864 BP.
XX AAVS9630;
AC
XX
DT 19-JAN-1999 (first entry)

XX
DE Human secreted protein gene 120 clone HGBGZ64.
XX
XX Human: secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
PN WO9839448-A2.
XX
PD 11-SEP-1998.
XX
PF 06-MAR-1998; 98WO-US04493.
XX
XX 02-OCT-1997; 97US-0061060.
PR 07-MAR-1997; 97US-0038621.
PR 07-MAR-1997; 97US-0040161.
PR 07-MAR-1997; 97US-0040162.
PR 07-MAR-1997; 97US-0040163.
PR 07-MAR-1997; 97US-0040333.
PR 07-MAR-1997; 97US-0040334.
PR 07-MAR-1997; 97US-0040336.
PR 07-MAR-1997; 97US-0040626.
PR 07-MAR-1997; 97US-0043311.
PR 11-APR-1997; 97US-0043312.
PR 11-APR-1997; 97US-0043313.
PR 11-APR-1997; 97US-0043314.
PR 11-APR-1997; 97US-0043569.
PR 11-APR-1997; 97US-0043576.
PR 11-APR-1997; 97US-0043578.
PR 11-APR-1997; 97US-0043580.
PR 11-APR-1997; 97US-0043669.
PR 11-APR-1997; 97US-0043670.
PR 11-APR-1997; 97US-0043671.
PR 11-APR-1997; 97US-0043672.
PR 11-APR-1997; 97US-0043674.
PR 11-APR-1997; 97US-0043742.
PR 23-MAY-1997; 97US-0047501.
PR 23-MAY-1997; 97US-0047502.
PR 23-MAY-1997; 97US-0047503.
PR 23-MAY-1997; 97US-0047581.
PR 23-MAY-1997; 97US-0047582.
PR 23-MAY-1997; 97US-0047584.
PR 23-MAY-1997; 97US-0047585.
PR 23-MAY-1997; 97US-0047586.
PR 23-MAY-1997; 97US-0047587.
PR 23-MAY-1997; 97US-0047588.
PR 23-MAY-1997; 97US-0047589.
PR 23-MAY-1997; 97US-0047590.
PR 23-MAY-1997; 97US-0047592.
PR 23-MAY-1997; 97US-0047593.
PR 23-MAY-1997; 97US-0047594.
PR 23-MAY-1997; 97US-0047595.
PR 23-MAY-1997; 97US-0047596.
PR 23-MAY-1997; 97US-0047597.
PR 23-MAY-1997; 97US-0047598.
PR 23-MAY-1997; 97US-0047599.
PR 23-MAY-1997; 97US-0047600.
PR 23-MAY-1997; 97US-0047601.
PR 23-MAY-1997; 97US-0047612.
PR 23-MAY-1997; 97US-0047613.
PR 23-MAY-1997; 97US-0047614.
PR 23-MAY-1997; 97US-0047615.
PR 23-MAY-1997; 97US-0047617.

CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 186
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAV9511 for described uses).

XX Sequence 1864 BP; 494 A; 403 C; 506 G; 455 T; 6 other:

QY	1	atggcgaccccaagcgtctcaaccacacacacggtctctatgtgccttgatcttgatagctat	60
Db	11	atggcgaccccaagcgtctctcgccccaagacacacacggtctcttggtgacagcttgatgattat	70
QY	61	aggtctgagcagaagaaggtatgtctctgtgtgagcttgcccttgggaagaagccacgcgcgac	120
Db	71	aagctcagagcagaagaaggttatgtctctgtgtgagcttgcccgagggaagagccacgactaac	130
QY	121	ccgctgtgaccaaagcactgcgggtctctggaacagagtttgagacccggttctccgcgcac	180
Db	131	ccgctgtgaccaaagcactgcgggcagcckxgagatgagttcgagaccgcgtctccgcgcac	190
QY	181	tctctcacccttgccgctcagctagctaaagctgagcccaagcgtctcaagccacgcttaac	240
Db	191	tctcctcagcttgccgctcagctagctaaagctgagcccaagcgtctcaagccacgcttaac	250
QY	241	caaggttccgacgaactttccaaagggtggccctcaactcgggtctgtgtgcatctctt	300
Db	251	caaggttccgacgaactttccaagggtggcccaactcgggtctgtgtgcatctctt	310
QY	301	gtctttggggcggtccctctgtgctgagagtgtaacaaagaatctgagcctttgtgtgga	360
Db	311	gtctttggggcggtccctctgtgctgagagtgtaacaaagaatctgagcctttgtgtgga	370
QY	361	caaggtcagaagatctgagtggtgacctcaactctggaacacgctctgctgacttgatccaaagc	420
Db	371	caaggtcagaagatctgagtggtgacctcaactctggaacacgctctgctgacttgatccaaagc	430
QY	421	aagtgacgagctg	432
Db	431	aagtgacgagctg	442

02-JUL-2001; 2001WO-EP07537

25.58; Score 148.4; DB 22; Length 150;

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Thu Jun 6 16:39:24 2002

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